

SEQUENCE LISTING

<110> Falco, S. Carl
Famodu, Layo O.
Orozco, Buddy
Schwaber, James S.

<120> Plant Aminoacyl-tRNA Synthetase

<130> BB-1193

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<150> 60/093,530
<151> July 21, 1998

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<213> Zea mays

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<213> Zea mays

<400> 2
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Pro Arg Leu Leu Gly Leu Ile Asp Ser Thr Thr Asn Trp Tyr Ile Arg
20 25 30

Phe Asn Arg Lys Arg Leu Lys Gly Glu Asn Gly Leu Asp Asp Thr Leu
35 40 45

His Ala Leu Asn Thr Leu Phe Glu Val Leu Phe Thr Leu Cys Arg Gly
50 55 60

Leu Ala Pro Phe Thr Pro Phe Leu Thr Asp Asn Ile Tyr Leu Lys Leu
65 70 75 80

Leu Pro His Ile Pro Lys Glu Leu Gln Ser Ala Asp Pro Arg Ser Val
85 90 95

His Phe Leu Pro Phe Pro Asp Val Arg Glu Glu Leu Phe Asp Glu Glu
100 105 110

Val Glu Arg Arg Val Gly Arg Met Gln Arg Val Ile Glu Leu Ala Arg
115 120 125

Val Ser Arg Glu Arg Arg Ala Ile Gly Leu Lys Gln Pro Leu Lys Thr
130 135 140

Leu Val Val Ile His Ser Asp Pro Gln Tyr Leu Glu Asp Val Lys Ser
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Leu Glu Lys Tyr Ile Ser Glu Glu Leu Asn Val Arg Asp Leu Val
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<212> DNA

<213> Oryza sativa

<220>

<221> unsure

<222> (386)

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<213> Oryza sativa

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Phe Ile Phe Tyr Asp Gly Pro Pro Phe Ala Thr Gly Leu Pro His Tyr
 35 40 45

Gly His Ile Leu Ala Gly Thr Ile Lys Asp Val Val Thr Arg His Gln
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Ser Met Arg Gly Arg His Val Ser Arg Arg Phe Xaa Trp Asp Cys His
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Gly Ser Pro

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 Ile Xaa Ser Ala Thr Gln Ser Leu Ile His Phe Val Arg Gln Glu Met
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 Asp Gly Tyr Arg Leu Tyr Thr Val Val Pro Tyr Leu Leu Lys Phe Leu
 35 40 45
 Asp Asn Leu Thr Asn Ile Tyr Val Arg Phe Asn Arg Lys Arg Leu Lys
 50 55 60
 Gly Arg Ser Gly Glu Glu Asp Cys Arg Ile Ala Leu Ser Thr Leu Tyr
 65 70 75 80
 His Val Leu Leu Ser Cys Lys Val Met Ala Pro Phe Thr Pro Phe
 85 90 95
 Phe Thr Glu Val Leu Tyr Gln Asn Met Arg
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 <211> 572
 <212> DNA
 <213> Triticum aestivum

<400> 7
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 ctcaagttcaa agggcgcacat gtcaaagagg ctgacaaggg tatcatcaat gctgttaagg 240
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 cgggcactcc tcttatttac cgggctttc caagctgggt tatcaagggtt gaaaagatca 360
 gggatcaattt actagaatgc aacaaggaga cctactgggt tccagattat gtcaaggaaa 420
 agagatttcca taactggcta gaaggtgctt gggactgggc tgtagcaga agtagattct 480
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<210> 8
 <211> 173
 <212> PRT
 <213> Triticum aestivum

<400> 8
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 Thr Gly Val Val His Cys Ala Pro Ala Phe Gly Glu Asp Asp His Arg
 20 25 30
 Val Cys Leu Ser Ala Gly Ile Ile Glu Ala Ser Gly Leu Val Val Ala
 35 40 45
 Val Asp Asp Asp Gly His Phe Ile Glu Lys Ile Ser Gln Phe Lys Gly
 50 55 60
 Arg His Val Lys Glu Ala Asp Lys Asp Ile Ile Asn Ala Val Lys Asp
 65 70 75 80

Lys Gly Arg Leu Val Ser Lys Gly Ser Ile Glu His Ser Tyr Pro Tyr
85 90 95

Cys Trp Arg Ser Gly Thr Pro Leu Ile Tyr Arg Ala Val Pro Ser Trp
100 105 110

Phe Ile Lys Val Glu Lys Ile Arg Asp Gln Leu Leu Glu Cys Asn Lys
115 120 125

Glu Thr Tyr Trp Val Pro Asp Tyr Val Lys Glu Lys Arg Phe His Asn
130 135 140

Trp Leu Glu Gly Ala Arg Asp Trp Ala Val Ser Arg Ser Arg Phe Trp
145 150 155 160

Gly Thr Pro Leu Pro Val Trp Ile Ser Gln Asp Gly Glu
165 170

<210> 9

<211> 2175

<212> DNA

<213> Zea mays

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<212> PRT
<213> Zea mays

<400> 10
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Gly Leu Glu Glu Lys Leu Ala Gly Leu Ser Thr Gly Gly Asp Gly Gln
35 40 45

Asn Pro Pro Pro Ala Gly Glu Gly Glu Glu Pro Gln Leu Ser Lys
50 55 60

Asn Ala Lys Lys Arg Glu Glu Lys Arg Lys Lys Leu Glu Glu Glu Arg
65 70 75 80

Arg Leu Lys Glu Glu Lys Lys Asn Lys Ala Ala Ala Ala Ser Gly
85 90 95

Lys Pro Gln Lys Ala Ser Ala Ala Asp Asp Asp Asp Met Asp Pro Thr
100 105 110

Gln Tyr Tyr Glu Asn Arg Leu Lys Ala Leu Asp Ser Leu Lys Ala Thr
115 120 125

Gly Val Asn Pro Tyr Pro His Lys Phe Pro Val Gly Ile Ser Val Pro
130 135 140

Glu Tyr Ile Glu Lys Tyr Arg Thr Leu Ser Glu Gly Glu Lys Leu Thr
145 150 155 160

Asp Val Ala Glu Cys Leu Ala Gly Arg Ile Met Asn Lys Arg Thr Ser
165 170 175

Ser Ser Lys Leu Phe Phe Tyr Asp Leu Tyr Gly Gly Met Lys Val
180 185 190

Gln Val Met Ala Asp Ala Arg Thr Ser Glu Leu Asp Glu Ala Glu Phe
195 200 205

Ser Lys Tyr His Ser Gly Val Lys Arg Gly Asp Ile Val Gly Ile Cys
210 215 220

Gly Tyr Pro Gly Lys Ser Asn Arg Gly Glu Leu Ser Val Phe Pro Lys
225 230 235 240

Arg Phe Val Val Leu Ser Pro Cys Leu His Met Met Pro Arg Gln Lys
245 250 255

Gly Glu Gly Ser Ala Val Pro Val Pro Trp Thr Pro Gly Met Gly Arg
260 265 270

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Arg	Tyr	Leu	Asp	Leu	Met	Val	Asn	His	Glu	Val	Arg	His	Ile	Phe	Lys
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Thr	Arg	Ser	Lys	Ile	Val	Ser	Phe	Ile	Arg	Lys	Phe	Leu	Asp	Asp	Arg
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Glu	Phe	Leu	Glu	Val	Glu	Thr	Pro	Met	Met	Asn	Met	Ile	Ala	Gly	Gly
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Ala	Ala	Ala	Arg	Pro	Phe	Val	Thr	His	His	Asn	Glu	Leu	Asn	Met	Arg
							340		345					350	
Leu	Phe	Met	Arg	Ile	Ala	Pro	Glu	Leu	Tyr	Leu	Lys	Glu	Leu	Val	Val
							355		360					365	
Gly	Gly	Leu	Asp	Arg	Val	Tyr	Glu	Ile	Gly	Lys	Gln	Phe	Arg	Asn	Glu
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Gly	Ile	Asp	Leu	Thr	His	Asn	Pro	Glu	Phe	Thr	Thr	Cys	Glu	Phe	Tyr
							385		390					400	
Met	Ala	Tyr	Ala	Asp	Tyr	Asn	Asp	Leu	Met	Glu	Leu	Thr	Glu	Thr	Met
							405		410					415	
Leu	Ser	Gly	Met	Val	Lys	Asp	Leu	Thr	Gly	Gly	Tyr	Ile	Lys	Tyr	
							420		425					430	
His	Ala	Asn	Gly	Val	Thr	Asn	Pro	Pro	Ile	Glu	Ile	Asp	Phe	Thr	Pro
							435		440					445	
Pro	Phe	Arg	Arg	Ile	Asp	Met	Ile	Lys	Asp	Leu	Glu	Ala	Met	Ala	Asn
							450		455					460	
Leu	Ser	Ile	Pro	Lys	Asp	Leu	Ser	Ser	Asp	Glu	Ala	Asn	Arg	Tyr	Leu
							465		470					480	
Ile	Glu	Ala	Cys	Val	Lys	Tyr	Asp	Val	Lys	Cys	Pro	Pro	Pro	Gln	Thr
							485		490					495	
Thr	Ser	Arg	Leu	Leu	Asp	Lys	Leu	Val	Gly	His	Phe	Leu	Glu	Glu	Thr
							500		505					510	
Cys	Val	Asn	Pro	Thr	Phe	Ile	Ile	Asn	His	Pro	Glu	Ile	Met	Ser	Pro
							515		520					525	
Leu	Ala	Lys	Trp	His	Arg	Ser	Arg	Pro	Gly	Leu	Thr	Glu	Arg	Phe	Glu
							530		535					540	
Leu	Phe	Val	Asn	Lys	His	Glu	Val	Cys	Asn	Ala	Tyr	Thr	Glu	Leu	Asn
							545		550					560	
Asp	Pro	Val	Val	Gln	Arg	Gln	Arg	Phe	Glu	Glu	Gln	Leu	Lys	Asp	Arg
							565		570					575	
Gln	Ser	Gly	Asp	Asp	Glu	Ala	Met	Ala	Leu	Asp	Glu	Thr	Phe	Cys	Thr
							580		585					590	

Ala Leu Glu Tyr Gly Leu Ala Pro Thr Gly Gly Trp Gly Leu Gly Ile
595 600 605

Asp Arg Leu Thr Met Leu Leu Thr Asp Ser Gln Asn Ile Lys Glu Val
610 615 620

Leu Leu Phe Pro Ala Met Lys Pro Gln Glu
625 630

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<213> Oryza sativa

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<210> 12
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 <213> Oryza sativa

<400> 12
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Ala Ala Ala Arg Pro Phe Val Thr His His Asn Glu Leu Asn Met Arg
 20 25 30

Leu Tyr Met Arg Ile Ala Pro Glu Leu Tyr Leu Lys Glu Leu Val Val
 35 40 45

Gly Gly Leu Asp Arg Val Tyr Glu Ile Gly Lys Gln Phe Arg Asn Glu
 50 55 60

Gly Ile Asp Leu Thr His Asn Pro Glu Phe Thr Thr Cys Glu Phe Tyr
 65 70 75 80

Met Ala Tyr Ala Asp Tyr Asn Asp Leu Ile Glu Leu Thr Glu Thr Met
 85 90 95

Leu Ser Gly Met Val Lys Glu Leu Thr Gly Gly Tyr Lys Ile Lys Tyr
 100 105 110

His Ala Asn Gly Val Glu Lys Pro Leu Asp Lys Leu Val
 115 120 125

<210> 13
 <211> 2143
 <212> DNA
 <213> Glycine max

<400> 13
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<210> 14
<211> 599
<212> PRT
<213> Glycine max

<220>
<221> UNSURE
<222> (392)...(393)...(394)

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35 40 45
Ala Lys Lys Ala Ala Glu Met Gln Lys Ala Lys Asp Asn Lys Ser Ala
50 55 60
Pro Ala Asp Glu Asp Asp Met Asp Pro Thr Gln Tyr Leu Glu Asn Arg
65 70 75 80
Leu Lys Tyr Leu Ala Val Gln Lys Ala Glu Gly Asn Asn Pro Tyr Pro
85 90 95
His Lys Phe Phe Val Thr Met Ser Leu Asp Gln Tyr Ile Lys Glu Tyr
100 105 110
Gly Gly Leu Ser Asn Gly Gln His Leu Glu Asp Val Ser Val Ser Met
115 120 125
Ala Gly Arg Ile Met His Lys Arg Thr Ser Gly Ser Lys Leu Val Phe
130 135 140
Tyr Asp Leu His Ser Gly Gly Phe Lys Val Gln Val Met Ala Asp Ala
145 150 155 160
Ser Lys Ser Asp Leu Asp Glu Ala Glu Phe Ser Lys Phe His Ser Asn
165 170 175
Val Lys Arg Gly Asp Ile Val Gly Ile Thr Gly Phe Pro Gly Lys Ser
180 185 190

Lys Lys Gly Glu Leu Ser Ile Phe Pro Lys Thr Phe Val Leu Leu Ser
195 200 205

His Cys Leu His Met Met Pro Arg Gln Lys Ser Ala Ala Ala Ala Asp
210 215 220

Asn Ala Asn Leu Lys Lys Asn Pro Trp Val Pro Gly Ser Thr Arg Asn
225 230 235 240

Pro Glu Thr Tyr Ile Leu Lys Asp Gln Glu Thr Arg Tyr Arg Arg His
245 250 255

Leu Asp Leu Met Leu Asn Pro Glu Val Arg Glu Ile Phe Lys Thr Arg
260 265 270

Ser Lys Ile Ile Cys Tyr Ile Arg Arg Phe Leu Asp Asp Leu Asp Phe
275 280 285

Leu Glu Val Glu Thr Pro Met Met Asn Met Ile Ala Gly Gly Ala Ala
290 295 300

Ala Arg Pro Phe Val Thr His His Asn Asp Leu Asn Met Arg Leu Phe
305 310 315 320

Met Arg Ile Ala Pro Glu Leu Tyr Leu Lys Glu Leu Val Val Gly Gly
325 330 335

Leu Asp Arg Val Tyr Glu Ile Gly Lys Gln Phe Arg Asn Glu Gly Ile
340 345 350

Asp Leu Thr His Asn Pro Glu Phe Thr Thr Cys Glu Phe Tyr Met Ala
355 360 365

Tyr Lys Asp Tyr Asn Asp Leu Met Asp Ile Thr Glu Gln Met Leu Ser
370 375 380

Gly Met Val Lys Glu Leu Thr Xaa Xaa Xaa Tyr Lys Ile Lys Tyr His
385 390 395 400

Ala Asp Gly Ile Asp Lys Glu Pro Ile Glu Ile Asp Phe Thr Pro Pro
405 410 415

Phe Arg Arg Ile Asp Met Ile Asp Glu Leu Glu Lys Val Ala Gly Leu
420 425 430

Ser Ile Pro Lys Asp Leu Ser Ser Glu Glu Ala Asn Gln Tyr Leu Lys
435 440 445

Asp Thr Cys Leu Lys Tyr Glu Ile Lys Cys Pro Pro Pro Glu Thr Thr
450 455 460

Ala Arg Leu Leu Asp Lys Leu Val Gly His Phe Leu Glu Glu Thr Cys
465 470 475 480

Val Asn Pro Thr Phe Ile Ile Asn His Pro Glu Ile Met Ser Pro Leu
485 490 495

Ala Lys Trp His Arg Ser Lys Arg Gly Leu Thr Glu Arg Phe Glu Leu
500 505 510

Phe Val Asn Lys His Glu Leu Cys Asn Ala Tyr Thr Glu Leu Asn Asp
 515 520 525
 Pro Val Val Gln Arg Gln Arg Phe Ala Glu Gln Leu Lys Asp Arg Gln
 530 535 540
 Ser Gly Asp Asp Glu Ala Met Ala Phe Asp Glu Thr Phe Cys Thr Ala
 545 550 555 560
 Leu Glu Tyr Gly Leu Pro Pro Thr Gly Gly Trp Gly Leu Gly Ile Asp
 565 570 575
 Arg Leu Thr Met Leu Leu Thr Asp Ser Gln Asn Ile Lys Glu Val Leu
 580 585 590
 Leu Phe Pro Ala Met Lys Pro
 595

<210> 15
 <211> 702
 <212> DNA
 <213> Triticum aestivum

<400> 15
 gacggaggct tgacaagcta gtggccatt tcttggagga aacatgtgtg aacccaacat 60
 ttattatcaa ccacccagag ataatgagtc cattggcaaa gtggcatagg tcccgacctg 120
 ggttgcacaga aaggtttgag ctctttgtta acaaacaacga ggtgtcaat gcctacactg 180
 agttgaacca caatgtttgtg caaaggcaac gtttggagga acaactaaag gatcgtcaat 240
 ctgtgtatga tgaagctatg gctttggacg aacattctg cactgccctc gagtatggc 300
 tgcctccgac aggtggttgg gtttggaa ttgatcgccc tacaatgtatg ctgacagatt 360
 cccagaacat caaggaagtt ctcttggttcc cgccatgaa gccccaaagag tagctgtttg 420
 caagcccatc aacagagtaa ttttggggat ctgcgttgag gttggaggat tatgacatgt 480
 gacaatacaa cgagtttaa ctgtgcggaa caaaacatgt gtagcagcac tggaggtaca 540
 agctacttt gcgtgaaagg gttgttggaaa atttgaactc cggttaggag gaagagttag 600
 gcatatgaag caagaatcag aaggagacag tggctacat gttgttggaaa ttctttttg 660
 gaagatcaaa atttagtgct tggattgtt atacactttt tt 702

<210> 16
 <211> 136
 <212> PRT
 <213> Triticum aestivum

<400> 16
 Thr Arg Leu Asp Lys Leu Val Gly His Phe Leu Glu Glu Thr Cys Val
 1 5 10 15
 Asn Pro Thr Phe Ile Ile Asn His Pro Glu Ile Met Ser Pro Leu Ala
 20 25 30
 Lys Trp His Arg Ser Arg Pro Gly Leu Thr Glu Arg Phe Glu Leu Phe
 35 40 45
 Val Asn Lys His Glu Val Cys Asn Ala Tyr Thr Glu Leu Asn Asp Pro
 50 55 60
 Val Val Gln Arg Gln Arg Phe Glu Glu Gln Leu Lys Asp Arg Gln Ser
 65 70 75 80
 Gly Asp Asp Glu Ala Met Ala Leu Asp Glu Thr Phe Cys Thr Ala Leu
 85 90 95

Glu Tyr Gly Leu Pro Pro Thr Gly Gly Trp Gly Leu Gly Ile Asp Arg
 100 105 110

Leu Thr Met Met Leu Thr Asp Ser Gln Asn Ile Lys Glu Val Leu Leu
115 120 125

Phe Pro Ala Met Lys Pro Gln Glu
130 135

1210 17
1211 1430
1212 DNA
1213 Zea m

<400>	17					
cgaaccgctc	gtctgtggcg	cctccgcgsg	cgtgttcgag	gcattggccac	gtttccaatg	6
ggcgctcccc	ccggcccat	ttcccccttc	accaccctcc	ccctctacta	tttttcgcgt	120
cgttcacccgc	gccttcgtgc	ccgttcttcc	tcggtcgctt	cggcacccgg	cggagcgaaa	180
gggcaccgac	cgcgccgctc	ccgggttgg	gtggggccgg	tcaagatcgc	gcgcgaggat	240
gttgtgaagg	aggatgtcc	gacaacaac	gtggccgaca	atatctttc	gaagatcgcc	300
ctgcagctgc	acaggaggga	taaccatccc	tttgggattt	tgaagaacac	aatttatgtat	360
taacttgaca	agaacttcac	tggggagttt	gacaaggttt	atgacctttt	ccctcttgc	420
tctgtcaaggc	agaattttga	tgtatgtctt	gtcccttctt	accatgttaag	ccggagttac	480
aaacgacacat	attatgtga	tggtcaaaca	gtttaaggt	gtcataccag	tgctcatcaa	540
gtcgagctgc	taaggcatgg	acatacacac	tttcttgtaa	ctggagatgt	ttaccgtagg	600
gattccatttgc	attcaactca	ctatctgtc	ttccatcaga	tggaaagggtt	ccgtgtcttc	660
tcttcgtatgt	aatggtcagg	gtctcgatg	gttgggacag	catacgacgc	tgcagaactc	720
aaagaaaaacac	tggaaaggctt	ggcaagacat	ctatttggt	ctgttagagat	gcgtatgggtt	780
gacacttact	tcccatttac	caaccatcc	tttggatctc	aaatataactt	tcaggatgtat	840
tggttggagg	ttttgggggt	tggagtcaac	gagcaggaaa	ttttgaaaag	aatggcagg	900
aggggaccatg	tggcatggc	ctttggattt	gytggagc	gccttgcata	ggtcctttc	960
gacattccat	atattcgact	attctggtc	aatgataaac	ggttcacgtc	ccagttctca	1020
gaaggcaagc	ttggtgtcaa	gttcaagcc	ttttcaaaat	ttcccttcgt	ttacaaggat	1080
atggatgttct	ggatcaatga	tgcatttaca	gaaaacaact	tatgtgaggt	tgtcagagga	1140
attgtcggt	atcttggtga	ggaggtaaaa	tttattgata	atttcacgaa	caagaaaggc	1200
atgacgagcc	attgtctata	aatggcttat	agggtcgatgg	aacgctcgct	cacagacgag	1260
gagattaaaca	atcttcgttt	gaatgtcagg	gaagctgtga	aagataaatt	ggaagttagag	1320
tttggatata	agcagctgc	tatgcagtt	taccatgaac	taaattttgc	ctctctttat	1380
atgtaaatcc	atttaaaatg	atttttttgt	atctatcaag	aaaatgcacc		1430

<210> 18
<211> 442
<212> PRT
<213> Zea mays

<400> 18
Arg Thr Ala Arg Cys Trp Leu Leu Arg Ala Arg Val Arg Gly Met Ala
1 5 10 15

Thr Leu Pro Met Ala Leu Ser Pro Ala Ala Ile Ser Pro Phe Thr Thr
20 25 30

Phe Phe Ser Val Ala Ser Ala Pro Gly Gly Ala Lys Gly His Arg Pro
50 55 60

Ala Ala Ser Ala Val Glu Val Gly Gly Val Lys Ile Ala Arg Glu Asp
 65 70 75 80
 Val Val Lys Glu Asp Asp Pro Thr Asn Asn Val Pro Asp Asn Ile Phe
 85 90 95
 Ser Lys Ile Gly Leu Gln Leu His Arg Arg Asp Asn His Pro Leu Gly
 100 105 110
 Ile Leu Lys Asn Thr Ile Tyr Asp Tyr Phe Asp Lys Asn Phe Thr Gly
 115 120 125
 Gln Phe Asp Lys Phe Asp Asp Leu Cys Pro Leu Val Ser Val Lys Gln
 130 135 140
 Asn Phe Asp Asp Val Leu Val Pro Ser Asp His Val Ser Arg Ser Tyr
 145 150 155 160
 Asn Asp Thr Tyr Tyr Val Asp Gly Gln Thr Val Leu Arg Cys His Thr
 165 170 175
 Ser Ala His Gln Ala Glu Leu Leu Arg His Gly His Thr His Phe Leu
 180 185 190
 Val Thr Gly Asp Val Tyr Arg Arg Asp Ser Ile Asp Ser Thr His Tyr
 195 200 205
 Pro Val Phe His Gln Met Glu Gly Phe Arg Val Phe Ser Pro Asp Glu
 210 215 220
 Trp Ser Gly Ser Arg Met Gly Gly Thr Ala Tyr Ala Ala Ala Glu Leu
 225 230 235 240
 Lys Lys Thr Leu Glu Gly Leu Ala Arg His Leu Phe Gly Ala Val Glu
 245 250 255
 Met Arg Trp Val Asp Thr Tyr Phe Pro Phe Thr Asn Pro Ser Phe Glu
 260 265 270
 Leu Glu Ile Tyr Phe Gln Asp Asp Trp Leu Glu Val Leu Gly Cys Gly
 275 280 285
 Val Thr Glu Gln Glu Ile Leu Lys Arg Asn Gly Arg Arg Asp His Val
 290 295 300
 Ala Trp Ala Phe Gly Leu Gly Leu Glu Arg Leu Ala Met Val Leu Phe
 305 310 315 320
 Asp Ile Pro Asp Ile Arg Leu Phe Trp Ser Asn Asp Lys Arg Phe Thr
 325 330 335
 Ser Gln Phe Ser Glu Gly Lys Leu Gly Val Lys Phe Lys Pro Phe Ser
 340 345 350
 Lys Phe Pro Pro Cys Tyr Lys Asp Met Ser Phe Trp Ile Asn Asp Ala
 355 360 365
 Phe Thr Glu Asn Asn Leu Cys Glu Val Val Arg Gly Ile Ala Gly Asp
 370 375 380

Leu Val Glu Glu Val Lys Leu Ile Asp Asn Phe Thr Asn Lys Lys Gly
390 395 400
385

Met Thr Ser His Cys Tyr Arg Ile Ala Tyr Arg Ser Met Glu Arg Ser
405 410 415
405

Leu Thr Asp Glu Glu Ile Asn Asn Leu Gln Leu Asn Val Arg Glu Ala
420 425 430
420

Val Lys Asp Lys Leu Glu Val Glu Leu Arg
435 440
435

<210> 19

<211> 1000

<212> DNA

<213> Oryza sativa

<400> 19
gcacgagttt taccaacagg atccctgtcg ggattcacac gatacatttt ttcttgaaac 60
ccctggccgt acaaaaacaat tgcctgaaga ttatctttagg aaagtaaagg aagttcatca 120
aagggtgggt tatggctcca agggatatgg ctatgactgg aaacgggatg aagcagagaa 180
aaacctgttt cgttaccacca ctacagcagt ttcaacaagg atgctataca agcttagcaca 240
aagaaaaacct tttggcccta agaggtacta ctccattgtat cgtgtttcc gcaatgaagc 300
tgtggaccgg actcatcttg cggaatttcca ccagattgaa ggttcatttt gtgattatgg 360
tttgcgtt ggtgatctga ttgggttattt ggaggatttc ttctcgagtc taggcattgtc 420
aaagctgcgt ttcaaggctt cctacaatcc atacaccggcc ccgagcatgg aaatttttag 480
ttaccatgaa gggttgaaga aatgggttggaa agttgttac acgttgcattt tcagacactga 540
aatgttactt cccatggggac tgccaggggg ttgttattttt attgtcatggg gtctttcaact 600
agaaaggcca acaatgatcc tttaggcattt cgacaacattt cgagacctct ttggaccaaa 660
qgttgcattt aacctcatca agagcaaccc tctctggccgc ttgggactgc agtaaaacct 720
tgcaaaagggtt ggttggaaat gattaatggaa caagattttt tttagtgcattt agtgggttggaa 780
cgttgcattt tcattttctgg cttacatttga aacaccaata catgtgcattt tagcagaggt 840
ttttgttattt cagtttttgcattt tgatatggaa ctaccaggcca attttttgtt gtgtccatatt 900
tcgaataactt tgatatactt taatttgcattt catccaaatgtt atgaaatggt catctggccgc 960
tgcgggttgcattt tgaatcaaaaa aaaaaaaaaaaaaaaa 1000

<210> 20

<211> 237

<212> PRT

<213> Oryza sativa

<400> 20
His Glu Trp Tyr Gln Gln His Pro Ala Arg Asp Ser His Asp Thr Phe
1 5 10 15

Phe Leu Glu Ala Pro Ala Ala Thr Lys Gln Leu Pro Glu Asp Tyr Leu
20 25 30

Glu Lys Val Lys Glu Val His Gln Arg Gly Gly Tyr Gly Ser Lys Gly
35 40 45

Tyr Gly Tyr Asp Trp Lys Arg Asp Glu Ala Glu Lys Asn Leu Leu Arg
50 55 60

Thr His Thr Thr Ala Val Ser Thr Arg Met Leu Tyr Lys Leu Ala Gln
65 70 75 80

Glu Lys Pro Phe Ala Pro Lys Arg Tyr Tyr Ser Ile Asp Arg Val Phe
85 90 95

Arg Asn Glu Ala Val Asp Arg Thr His Leu Ala Glu Phe His Gln Ile
100 105 110

Glu Gly Leu Ile Cys Asp Tyr Gly Leu Thr Leu Gly Asp Leu Ile Gly
115 120 125

Val Leu Glu Asp Phe Phe Ser Ser Leu Gly Met Ser Lys Leu Arg Phe
130 135 140

Lys Pro Ala Tyr Asn Pro Tyr Thr Glu Pro Ser Met Glu Ile Phe Ser
145 150 155 160

Tyr His Glu Gly Leu Lys Lys Trp Val Glu Val Gly Asn Ser Gly Met
165 170 175

Phe Arg Pro Glu Met Leu Leu Pro Met Gly Leu Pro Glu Gly Val Asn
180 185 190

Val Ile Ala Trp Gly Leu Ser Leu Glu Arg Pro Thr Met Ile Leu Tyr
195 200 205

Gly Ile Asp Asn Ile Arg Asp Leu Phe Gly Pro Lys Val Asp Phe Asn
210 215 220

Leu Ile Lys Ser Asn Pro Leu Cys Arg Leu Gly Leu Gln
225 230 235

<210> 21
<211> 387
<212> DNA
<213> Glycine max

<220>
<221> unsure
<222> (337)

<220>
<221> unsure
<222> (379)

<400> 21
gattgccaat ggatcatgga aagaaaaatc attcaaattct ttgaattttag gaaaaggagt 60
catgggtgtc cctccaaatg gtggccatct tcacacttta cttaaatgca gaactatgat 120
gaaagaaaatc ttcttgaaaa tgggatttga agaaatgcca accaacaatt acgttgaatc 180
ttctttctgg aattttgata ctttatttca acctcaacaa catcctgctc gtgatgctca 240
cgatacttgc ttcccttctg aacctgcattc tgccaaatcc attccacaag attatttaga 300
aagagtgaaa acaatgcattg agaaaggagg gcacggntct attgggtgga gatacgaatc 360
gagtggaaac tgagtccana aaaaaaaa 387

<210> 22
<211> 123
<212> PRT
<213> Glycine max

<400> 22
Ile Ala Asn Gly Ser Trp Lys Glu Lys Ser Phe Lys Ser Leu Asn Leu
1 5 10 15
Gly Lys Gly Val Met Gly Val Pro Pro Asn Gly Gly His Leu His Thr
20 25 30

Leu Leu Lys Cys Arg Thr Met Met Lys Glu Ile Phe Leu Glu Met Gly
 35 40 45
 Phe Glu Glu Met Pro Thr Asn Asn Tyr Val Glu Ser Ser Phe Trp Asn
 50 55 60
 Phe Asp Thr Leu Phe Gln Pro Gln Gln His Pro Ala Arg Asp Ala His
 65 70 75 80
 Asp Thr Phe Phe Leu Ser Glu Pro Ala Ser Ala Lys Ser Ile Pro Gln
 85 90 95
 Asp Tyr Leu Glu Arg Val Lys Thr Met His Glu Lys Gly Gly His Gly
 100 105 110
 Ser Ile Gly Trp Arg Tyr Asp Trp Ser Gly Asn
 115 120

<210> 23
 <211> 1074
 <212> DNA
 <213> Triticum aestivum

<400> 23
 gcacgaggga caacctatty ctagatggata tagccaaccg ttgttagagg tccgtgaggc 60
 aatccagaac attttctcg agatgggtt cagttagatg ccaacgaaca tgtatgtaga 120
 gagcagcttc tggaaatttg atgcactgtt ccagccacaa cagcatctg ctctgtgatc 180
 aacgatacc ttttctca aagccctgtc tacaacaaca caattacctg atgactatct 240
 tgagaaatgt aagcaagtac atcgtctgg tggatcatggc tccaaaggat atggttacg 300
 ttggaaagcga gatgaagcag agaaaaaacct gttcgact cacacaactg cagttcaac 360
 aaggatgcta tacaagctag cacaggagaa aactttgtctt ctaaagat actattctat 420
 tgatcgtgtt ttccggaatg aagctgtggc cccaaactcat ttgcagaat tccaccagat 480
 agaaggcttt atttgtgatt atggtttgc gttggtgat ctgataggtg tattggagga 540
 tttcttctcc agactaggca tgcataaactg gctttcaaa cctgcctaca acccgtagac 600
 tgaaccaagc atggaaattt tcagctacca cgttgtctg aagaaatggg tggaaatagg 660
 caactcagcc atgttcaggc cggaaatgtt acttcccattt ggactgccag agggtgttaa 720
 tggatcgca tgggttctt cgttggaaatg gccaacaatg attctgtatg ggattgacaa 780
 catacgttat ctctttgggc caaaggtcgat cttcaatctg atcaagagca gcccgttttg 840
 cccgttgggg ctgtatgtt gtgagcttga tagaacttta tctggatgtc tggatgcgaa 900
 ggtatgttat ttgtggttat accttgaaa accagtactt gtgcattaa cagagggagt 960
 gcagaaatac acacatgtatc ctctgaattt caaaaaaaaaaaaaaa aaaaaaaaaaaa 1020
 aataaaaaaaaaaa aaacaaaaaaaaaa tactcgaggg gggccgtac caca 1074

<210> 24
 <211> 284
 <212> PRT
 <213> Triticum aestivum

<400> 24
 His Glu Gly Gln Pro Ile Ala Ile Gly Tyr Ser Gln Pro Leu Leu Glu
 1 5 10 15
 Val Arg Glu Ala Ile Gln Asn Ile Phe Leu Glu Met Gly Phe Ser Glu
 20 25 30
 Met Pro Thr Asn Met Tyr Val Glu Ser Ser Phe Trp Asn Phe Asp Ala
 35 40 45

Leu Phe Gln Pro Gln Gln His Pro Ala Arg Asp Ser His Asp Thr Phe
 50 55 60
 Phe Leu Lys Ala Pro Ala Thr Thr Thr Gln Leu Pro Asp Asp Tyr Leu
 65 70 75 80
 Glu Lys Val Lys Gln Val His Gln Ser Gly Gly His Gly Ser Lys Gly
 85 90 95
 Tyr Gly Tyr Asp Trp Lys Arg Asp Glu Ala Glu Lys Asn Leu Leu Arg
 100 105 110
 Thr His Thr Thr Ala Val Ser Thr Arg Met Leu Tyr Lys Leu Ala Gln
 115 120 125
 Glu Lys Thr Phe Ala Pro Lys Arg Tyr Tyr Ser Ile Asp Arg Val Phe
 130 135 140
 Arg Asn Glu Ala Val Asp Arg Thr His Leu Ala Glu Phe His Gln Ile
 145 150 155 160
 Glu Gly Leu Ile Cys Asp Tyr Gly Leu Thr Leu Gly Asp Leu Ile Gly
 165 170 175
 Val Leu Glu Asp Phe Ser Arg Leu Gly Met Ser Lys Leu Arg Phe
 180 185 190
 Lys Pro Ala Tyr Asn Pro Tyr Thr Glu Pro Ser Met Glu Ile Phe Ser
 195 200 205
 Tyr His Asp Gly Leu Lys Lys Trp Val Glu Ile Gly Asn Ser Gly Met
 210 215 220
 Phe Arg Pro Glu Met Leu Leu Pro Met Gly Leu Pro Glu Gly Val Asn
 225 230 235 240
 Val Ile Ala Trp Gly Leu Ser Leu Glu Arg Pro Thr Met Ile Leu Tyr
 245 250 255
 Gly Ile Asp Asn Ile Arg Asp Leu Phe Gly Pro Lys Val Asp Phe Asn
 260 265 270
 Leu Ile Lys Ser Ser Pro Ile Cys Arg Leu Gly Leu
 275 280

<210> 25
 <211> 1939
 <212> DNA
 <213> Zea mays

<400> 25
 gtccggatt cccgggtcga cccacgcgtc cgtgctgtcc cattggcaac ttgcgcgcta 60
 ctctgactcg agtggccgt actctacccc acccacaccc ttccgcggc cgccactaaa 120
 ccctagcggg acaccccgct tgctcgccg ccctcatctc ctcactcctc tcggaccggc 180
 ggtggccgtt gcagagctgc gcgjaccgaga accgaatctg tgagccatgt cgaccaacaa 240
 gggcagcgcg gccaaggccg gcccggggaa gaagaaggag gtgaagaagg agacgaagct 300
 gggatggcc tataagaagg acgacaactt cggggatgtt tactccgagg ttgttgttaa 360
 cagtgaaatg attgagttact atgacattc tgggtgttat atattgaggc catggcgat 420
 ggaaatctgg gagctactga aagaattctt tgatgcagaa attaaaaagc tgaagctcaa 480
 accatattat ttccctttgt ttgttactga gaatgttcta cagaaggaaa aggaccat 540

tgagggctt gcacctgagg tagttgggt tactaaatct gggaaatctg acctggaaagc 600
 acccgattgca atccgcacca caagtggagac tgcgtatgtat ccgtacttct ccaaataatggat 660
 aagaagccac cgagacttac ccttgagggtg taatcaatgg tggtaatgttgg ttagatggga 720
 gtttagcaat ccaacttct tcataaggag cctgtgaatt ctgtggcaag aggggcataac 780
 tggtttgcg actaaagaag aggcatgtg agagggtctc caaatattgg aactgtaccg 840
 aaggatatac gaagaatttt tagcgttcc agttccaaa gggagaaaaa gcgagatgg 900
 aaaatttgcg ggtggcctt ataccacca cgttgaggcc ttcatccaa acactggtcg 960
 tggcatacaa ggcgcacact casactgtct tggtaaaaac ttgcacaaga tggttgatata 1020
 casttttag aatgagaaag gtgttaggaa aatgggttgg caaaacttctt ggcctacac 1080
 aacccgctcg attggagtga tggatgac acatgggtat gacaaaggct tagtattacc 1140
 accaaagggtg gcaccaatcc aggttaatctg gatttcgtg ccttataagg acgctgacac 1200
 aactgcccata aaggggaccc gcaaatcaac tggttacaca ctgcataat ctgggattag 1260
 agcggatcatg gacaccctgt aaaattactc tcaggttgg aagtattccc actgggaaat 1320
 gaaagggtgtt ccattgagaa ttgagattgg tccaaaagat ctggcaaaaca aacagggtcg 1380
 tgggtccgc cggacaacg gtgcaaaagg tgacatccct gtgaccaatt tggttgaaga 1440
 ggtaaagtgtt tactggat agattcaaaa aaatctgttc aaaacagccc aagaaaaagag 1500
 agatgcctgt gttcatgtcg tgaacacttq qgatgaattt acaactgtct tgaataacaa 1560
 aaagttgatc ttgycatccat ggtgtatga ggaggaaatt gagaaagatg taaaaactcg 1620
 gacaaaagggg gaacttggag ctgcgaaaaac atttgtact ccatttgagc agccagaact 1680
 tccagaaggtt accctgtctt tgcatactgg aagccagcg aagaagtgtt cgttctgggg 1740
 cccragctac tgattgcctg tgctggatt atttctggat tcaagtcttag tgagttatgt 1800
 aqetttgaag tgcggatac aaatccaaa atccatttac attgcgtttt acatcgactt 1860
 gcagttctca tgcatactact gctgacaaaaa gcatcgatt tccctgtggac catgctattc 1920
 gagtttgaat gttgcaagg 1939

<210> 26
 <211> 383
 <212> PRT
 <213> Zea mays

<400> 26
 Pro Ile Ala Ile Arg Pro Thr Ser Glu Thr Val Met Tyr Pro Tyr Phe
 1 5 10 15
 Ser Lys Trp Ile Arg Ser His Arg Asp Leu Pro Leu Arg Cys Asn Gln
 20 25 30
 Trp Cys Asn Val Val Arg Trp Glu Phe Ser Asn Pro Thr Pro Phe Ile
 35 40 45
 Arg Ser Arg Glu Phe Leu Trp Gln Glu Gly His Thr Ala Phe Ala Thr
 50 55 60
 Lys Glu Glu Ala Asp Glu Glu Val Leu Gln Ile Leu Glu Leu Tyr Arg
 65 70 75 80
 Arg Ile Tyr Glu Glu Phe Leu Ala Val Pro Val Ser Lys Gly Arg Lys
 85 90 95
 Ser Glu Met Glu Lys Phe Ala Gly Gly Leu Tyr Thr Thr Ser Val Glu
 100 105 110
 Ala Phe Ile Pro Asn Thr Gly Arg Gly Ile Gln Gly Ala Thr Ser His
 115 120 125
 Cys Leu Gly Gln Asn Phe Ala Lys Met Phe Asp Ile Thr Phe Glu Asn
 130 135 140
 Glu Lys Gly Val Arg Glu Met Val Trp Gln Asn Ser Trp Ala Tyr Thr
 145 150 155 160

Thr Arg Ser Ile Gly Val Met Val Met Thr His Gly Asp Asp Lys Gly
 165 170 175
 Leu Val Leu Pro Pro Lys Val Ala Pro Ile Gln Val Ile Val Ile Ser
 180 185 190
 Val Pro Tyr Lys Asp Ala Asp Thr Thr Ala Ile Lys Gly Ala Cys Glu
 195 200 205
 Ser Thr Val Tyr Thr Leu Asp Gln Ser Gly Ile Arg Ala Asp Gln Asp
 210 215 220
 Thr Arg Glu Asn Tyr Ser Pro Gly Trp Lys Tyr Ser His Trp Glu Met
 225 230 235 240
 Lys Gly Val Pro Leu Arg Ile Glu Ile Gly Pro Lys Asp Leu Ala Asn
 245 250 255
 Lys Gln Val Arg Val Val Arg Asp Asn Gly Ala Lys Val Asp Ile
 260 265 270
 Pro Val Thr Asn Leu Val Glu Glu Val Lys Val Leu Leu Asp Glu Ile
 275 280 285
 Gln Lys Asn Leu Phe Lys Thr Ala Gln Glu Lys Arg Asp Ala Cys Val
 290 295 300
 His Val Val Asn Thr Trp Asp Glu Phe Thr Thr Ala Leu Asn Asn Lys
 305 310 315 320
 Lys Leu Ile Leu Ala Pro Trp Cys Asp Glu Glu Glu Ile Glu Lys Asp
 325 330 335
 Val Lys Thr Arg Thr Lys Gly Glu Leu Gly Ala Ala Lys Thr Leu Cys
 340 345 350
 Thr Pro Phe Glu Gln Pro Glu Leu Pro Glu Gly Thr Leu Cys Phe Ala
 355 360 365
 Ser Gly Lys Pro Ala Lys Lys Trp Ser Phe Trp Gly Arg Ser Tyr
 370 375 380

<210> 27
 <211> 697
 <212> DNA
 <213> Glycine max

<220>
 <221> unsure
 <222> (11)

<226>
 <221> unsure
 <222> (40)

<220>
 <221> unsure
 <222> (42)

<220>
<221> unsure
<222> (91)

<220>
<221> unsure
<222> (118)

<220>
<221> unsure
<222> (183)

<220>
<221> unsure
<222> (266)

<220>
<221> unsure
<222> (304)

<220>
<221> unsure
<222> (503)

<220>
<221> unsure
<222> (632)

<220>
<221> unsure
<222> (694)

<400> 27
gtggaaacagt natgtatccc tactactcta agtggataan gngacatcg t gacttgcctt 60
tggaaactaa tcagtttgtc aatgttgtaa natgggagtt cagcaacccc actccatnca 120
tcaggagtc cgagtttctt tggcaagaag ggcacactgc ttttgcaca aaggatgaag 180
canatgcaga agttcttgag attctggat tatataggcg tatatacgaa gagtattttgg 240
cagttccctgt catabagggt aagaanagtg agcttgagaa gtttgcgtgt ggactctaca 300
ctaaaaatgt tgaggcattt attccaaaca ctggtcgtgg tatccaaagggt gcaacttctc 360
attgttttggg cccaaaatttt gctaaaaatgt ttgagataaa ctttggaaaat gaaaaggagg 420
agaaaagcaat ggtctggcag aattcatggg cctatagtagtac tcgaactatt ggggtcatgg 480
tgatggttca tggtgatgac aangggattt gtactacctc ctaaagtagc atcagtacaa 540
gttatttgta ttccctgtgcc ttacaaagat gccgatactc aaggaatctt tgatgcctgt 600
ctgcactgtg aatacattga tgaagcagga tngcgttag cagatctaga gatatatctc 660
ctggatgaga tccactggga atgaaagggt ctcnaga 697

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<212> PRT
<213> Glycine max

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Asp Leu Pro Leu Lys Leu Asn Gln Trp Cys Asn Val Val Xaa Trp Glu
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Phe Ser Asn Pro Thr Pro Xaa Ile Arg Ser Arg Glu Phe Leu Trp Gln
35 40 45
Glu Gly His Thr Ala Phe Ala Thr Lys Asp Glu Ala Xaa Ala Glu Val
50 55 60
Leu Glu Ile Leu Glu Leu Tyr Arg Arg Ile Tyr Glu Glu Tyr Leu Ala
65 70 75 80
Val Pro Val Ile Lys Gly Lys Xaa Ser Glu Leu Glu Lys Phe Ala Gly
85 90 95
Gly Leu Tyr Thr Xaa Asn Val Glu Ala Phe Ile Pro Asn Thr Gly Arg
100 105 110
Gly Ile Gln Gly Ala Thr Ser His Cys Leu Gly Gln Asn Phe Ala Lys
115 120 125
Met Phe Glu Ile Asn Phe Glu Asn Glu Lys Gly Glu Lys Ala Met Val
130 135 140
Trp Gln Asn Ser Trp Ala Tyr Ser Thr Arg Thr Ile Gly Val Met Val
145 150 155 160
Met Val His Gly Asp Asp Xaa Gly Ile Gly Thr Thr Ser
165 170

<210> 29
<211> 564
<212> DNA
<213> Triticum aestivum

<220>
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<222> (564)

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aatatatgaa gaatttttag cagttccagt gtccaaaggg aggaaaagtg agatggaaaa 180
gtttgttgtt ggactttata caaccagtgt agaggccttc attccaaata ctggccgtgg 240
tatacaaggt gcaacttcac attgtcttgg tcaaaacttt gcaaagatgt ttgatatcac 300
tttcgagaat gaaaagggtg aacggtccat ggtgtggcag aactctygg catacaactac 360
ccgtctcgatt ggggtcatga taatgacaca tyyltgatgac aagggcttag tgcgtgccacc 420
aaaggtgacc tatecaggnc attgtatcct gtgccattaa agatgntgac acaacagcta 480
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qaaatacccc caggtggaaa atcn 564

<210> 30
<211> 152
<212> PRT
<213> Triticum aestivum

<400> 30
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Gly His Thr Val Phe Ala Thr Lys Glu Glu Ala Asp Glu Glu Val Leu
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Gln Ile Leu Glu Leu Tyr Arg Arg Ile Tyr Glu Glu Phe Leu Ala Val
35 40 45
Pro Val Ser Lys Gly Arg Lys Ser Glu Met Glu Lys Phe Ala Gly Gly
50 55 60
Leu Tyr Thr Thr Ser Val Glu Ala Phe Ile Pro Asn Thr Gly Arg Gly
65 70 75 80
Ile Gln Gly Ala Thr Ser His Cys Leu Gly Gln Asn Phe Ala Lys Met
85 90 95
Phe Asp Ile Thr Phe Glu Asn Glu Lys Gly Glu Arg Ser Met Val Trp
100 105 110

Gln Asn Ser Trp Ala Tyr Thr Thr Arg Ser Ile Gly Val Met Ile Met
 115 120 125
 Thr His Gly Asp Asp Lys Gly Leu Val Leu Pro Pro Lys Val Thr Tyr
 130 135 140
 Pro Gly His Cys Ile Leu Cys His
 145 150
 <210> 31
 <211> 1072
 <212> PRT
 <213> *Saccharomyces cerevisiae*
 <400> 31
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 Val Leu Ser Leu Trp Asp Glu Ile Asp Ala Phe His Thr Ser Leu Glu
 20 25 30
 Leu Thr Lys Asp Lys Pro Glu Phe Ser Phe Asp Gly Pro Pro Phe
 35 40 45
 Ala Thr Gly Thr Pro His Tyr Gly His Ile Leu Ala Ser Thr Ile Lys
 50 55 60
 Asp Ile Val Pro Arg Tyr Ala Thr Met Thr Gly His His Val Glu Arg
 65 70 75 80
 Arg Phe Gly Trp Asp Thr His Gly Val Pro Ile Glu His Ile Ile Asp
 85 90 95
 Lys Lys Leu Gly Ile Thr Gly Lys Asp Asp Val Phe Lys Tyr Gly Leu
 100 105 110
 Glu Asn Tyr Asn Asn Glu Cys Arg Ser Ile Val Met Thr Tyr Ala Ser
 115 120 125
 Asp Trp Arg Lys Thr Ile Gly Arg Leu Gly Arg Trp Ile Asp Phe Asp
 130 135 140
 Asn Asp Tyr Lys Thr Met Tyr Pro Ser Phe Met Glu Ser Thr Trp Trp
 145 150 155 160
 Ala Phe Lys Gln Leu His Glu Lys Gly Gln Val Tyr Arg Gly Phe Lys
 165 170 175
 Val Met Pro Tyr Ser Thr Gly Leu Thr Thr Pro Leu Ser Asn Phe Glu
 180 185 190
 Ala Gln Gln Asn Tyr Lys Asp Val Asn Asp Pro Ala Val Thr Ile Gly
 195 200 205
 Phe Asn Val Ile Gly Gln Glu Lys Thr Gln Leu Val Ala Trp Thr Thr
 210 215 220
 Thr Pro Trp Thr Leu Pro Ser Asn Leu Ser Leu Cys Val Asn Ala Asp
 225 230 235 240

Phe Glu Tyr Val Lys Ile Tyr Asp Glu Thr Arg Asp Arg Tyr Phe Ile
 245 250 255
 Leu Leu Glu Ser Leu Ile Lys Thr Leu Tyr Lys Lys Pro Lys Asn Glu
 260 265 270
 Lys Tyr Lys Ile Val Glu Lys Ile Lys Gly Ser Asp Leu Val Gly Leu
 275 280 285
 Lys Tyr Glu Pro Leu Phe Pro Tyr Phe Ala Glu Gln Phe His Glu Thr
 290 295 300
 Ala Phe Arg Val Ile Ser Asp Asp Tyr Val Thr Ser Asp Ser Gly Thr
 305 310 315 320
 Gly Ile Val His Asn Ala Pro Ala Phe Gly Glu Glu Asp Asn Ala Ala
 325 330 335
 Cys Leu Lys Asn Gly Val Ile Ser Glu Asp Ser Val Leu Pro Asn Ala
 340 345 350
 Ile Asp Asp Leu Gly Arg Phe Thr Lys Asp Val Pro Asp Phe Glu Gly
 355 360 365
 Val Tyr Val Lys Asp Ala Asp Lys Leu Ile Ile Lys Tyr Leu Thr Asn
 370 375 380
 Thr Gly Asn Leu Leu Leu Ala Ser Gin Ile Arg His Ser Tyr Pro Phe
 385 390 395 400
 Cys Trp Arg Ser Asp Thr Pro Leu Leu Tyr Arg Ser Val Pro Ala Trp
 405 410 415
 Phe Val Arg Val Lys Asn Ile Val Pro Gln Met Leu Asp Ser Val Met
 420 425 430
 Lys Ser His Trp Val Pro Asn Thr Ile Lys Glu Lys Arg Phe Ala Asn
 435 440 445
 Trp Ile Ala Asn Ala Arg Asp Trp Asn Val Ser Arg Asn Arg Tyr Trp
 450 455 460
 Gly Thr Pro Ile Pro Leu Trp Val Ser Asp Asp Phe Glu Glu Val Val
 465 470 475 480
 Cys Val Gly Ser Ile Lys Glu Leu Glu Leu Thr Gly Val Arg Asn
 485 490 495
 Ile Thr Asp Leu His Arg Asp Val Ile Asp Lys Leu Thr Ile Pro Ser
 500 505 510
 Lys Gln Gly Lys Gly Asp Leu Lys Arg Ile Glu Glu Val Phe Asp Cys
 515 520 525
 Trp Phe Glu Ser Gly Ser Met Pro Tyr Ala Ser Gln His Tyr Pro Phe
 530 535 540
 Glu Asn Thr Glu Lys Phe Asp Glu Arg Val Pro Ala Asn Phe Ile Ser
 545 550 555 560

Glu Gly Leu Asp Gln Thr Arg Gly Trp Phe Tyr Thr Leu Ala Val Leu
 565 570 575
 Gly Thr His Leu Phe Gly Ser Val Pro Tyr Lys Asn Val Ile Val Ser
 580 585 590
 Gly Ile Val Leu Ala Ala Asp Gly Arg Lys Met Ser Lys Ser Leu Lys
 595 600 605
 Asn Tyr Pro Asp Pro Ser Ile Val Leu Asn Lys Tyr Gly Ala Asp Ala
 610 615 620
 Leu Arg Leu Tyr Leu Ile Asn Ser Pro Val Leu Lys Ala Glu Ser Leu
 625 630 640
 Lys Phe Lys Glu Glu Gly Val Lys Glu Val Val Ser Lys Val Leu Leu
 645 650 655
 Pro Trp Trp Asn Ser Phe Lys Phe Leu Asp Gly Gln Ile Ala Leu Leu
 660 665 670
 Lys Lys Met Ser Asn Ile Asp Phe Gln Tyr Asp Asp Ser Val Lys Ser
 675 680 685
 Asp Asn Val Met Asp Arg Trp Ile Leu Ala Ser Met Gln Ser Leu Val
 690 695 700
 Gln Phe Ile His Glu Glu Met Gly Gln Tyr Lys Leu Tyr Thr Val Val
 705 710 715 720
 Pro Lys Leu Leu Asn Phe Ile Asp Glu Leu Thr Asn Trp Tyr Ile Arg
 725 730 735
 Phe Asn Arg Arg Arg Leu Lys Gly Glu Asn Gly Val Glu Asp Cys Leu
 740 745 750
 Lys Ala Leu Asn Ser Leu Phe Asp Ala Leu Phe Thr Phe Val Arg Ala
 755 760 765
 Met Ala Pro Phe Thr Pro Phe Leu Ser Glu Ser Ile Tyr Leu Arg Leu
 770 775 780
 Lys Glu Tyr Ile Pro Glu Ala Val Leu Ala Lys Tyr Gly Lys Asp Gly
 785 790 795 800
 Arg Ser Val His Phe Leu Ser Tyr Pro Val Val Lys Lys Glu Tyr Phe
 805 810 815
 Asp Glu Ala Ile Glu Thr Ala Val Ser Arg Met Gln Ser Val Ile Asp
 820 825 830
 Leu Gly Arg Asn Ile Arg Glu Lys Lys Thr Ile Ser Leu Lys Thr Pro
 835 840 845
 Leu Lys Thr Leu Val Ile Leu His Ser Asp Glu Ser Tyr Leu Lys Asp
 850 855 860
 Val Glu Ala Leu Lys Asn Tyr Ile Glu Glu Leu Asn Val Arg Asp
 865 870 875 880

Val Val Ile Thr Ser Asp Glu Ala Lys Tyr Gly Val Glu Tyr Lys Ala
 885 890 895
 Val Ala Asp Trp Pro Val Leu Gly Lys Lys Leu Lys Lys Asp Ala Lys
 900 905 910
 Lys Val Lys Asp Ala Leu Pro Ser Val Thr Ser Glu Gln Val Arg Glu
 915 920 925
 Tyr Leu Glu Ser Gly Lys Leu Gln Val Ala Gly Ile Glu Leu Val Lys
 930 935 940
 Gly Asp Leu Asn Ala Ile Arg Gly Leu Pro Glu Ser Ala Val Gln Ala
 945 950 955 960
 Gly Gln Glu Thr Arg Thr Asp Gln Asp Val Leu Ile Ile Met Asp Thr
 965 970 975
 Asn Ile Tyr Ser Glu Leu Lys Ser Glu Gly Leu Ala Arg Glu Leu Val
 980 985 990
 Asn Arg Ile Gln Lys Leu Arg Lys Lys Cys Gly Leu Glu Ala Thr Asp
 995 1000 1005
 Asp Val Leu Val Glu Tyr Glu Leu Val Lys Asp Thr Ile Asp Phe Glu
 1010 1015 1020
 Ala Ile Val Lys Glu His Phe Asp Met Leu Ser Lys Thr Cys Arg Ser
 1025 1030 1035 1040
 Asp Ile Ala Lys Tyr Asp Gly Ser Lys Thr Asp Pro Ile Gly Asp Glu
 1045 1050 1055
 Glu Gln Ser Ile Asn Asp Thr Ile Phe Lys Leu Lys Val Phe Lys Leu
 1060 1065 1070
 <210> 32
 <211> 1266
 <212> PRT
 <213> Homo sapiens

 <400> 32
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 20 25 30
 Gln Glu Cys Leu Lys Gln Ser Lys His Lys Pro Lys Phe Thr Phe Tyr
 35 40 45
 Asp Gly Pro Pro Phe Ala Thr Gly Leu Pro His Tyr Gly His Ile Leu
 50 55 60
 Ala Gly Thr Ile Lys Asp Ile Val Thr Arg Tyr Ala His Gln Ser Gly
 65 70 75 80
 Phe His Val Asp Arg Arg Phe Gly Trp Asp Cys His Gly Leu Pro Val
 85 90 95

Glu Tyr Glu Ile Asp Lys Thr Leu Gly Ile Arg Gly Pro Glu Asp Val
100 105 110
Ala Lys Met Gly Ile Thr Glu Tyr Asn Asn Gln Cys Arg Ala Ile Val
115 120 125
Met Arg Tyr Ser Ala Glu Trp Lys Ser Thr Val Ser Arg Leu Gly Arg
130 135 140
Trp Ile Asp Phe Asp Asn Asp Tyr Lys Thr Leu Tyr Pro Gln Phe Met
145 150 155 160
Glu Ser Val Trp Trp Val Phe Lys Gln Leu Tyr Asp Lys Gly Leu Val
165 170 175
Tyr Arg Gly Val Lys Val Met Pro Phe Ser Thr Ala Cys Asn Thr Pro
180 185 190
Leu Ser Asn Phe Glu Ser His Gln Asn Tyr Lys Asp Val Gln Asp Pro
195 200 205
Ser Val Phe Val Thr Phe Pro Leu Glu Glu Asp Glu Thr Val Ser Leu
210 215 220
Val Ala Trp Thr Thr Pro Trp Thr Leu Pro Ser Asn Leu Ala Val
225 230 235 240
Cys Val Asn Pro Glu Met Gln Tyr Val Lys Ile Lys Asp Val Ala Arg
245 250 255
Gly Arg Leu Leu Ile Leu Met Glu Ala Arg Leu Ser Ala Leu Tyr Lys
260 265 270
Leu Glu Ser Asp Tyr Glu Ile Leu Glu Arg Phe Pro Gly Ala Tyr Leu
275 280 285
Lys Gly Lys Lys Tyr Arg Pro Leu Phe Asp Tyr Phe Leu Lys Cys Lys
290 295 300
Glu Asn Gly Ala Phe Thr Val Leu Val Asp Asn Tyr Val Lys Glu
305 310 315 320
Glu Gly Thr Gly Val Val His Gln Ala Pro Tyr Phe Gly Ala Glu Asp
325 330 335
Tyr Arg Val Cys Met Asp Phe Asn Ile Ile Arg Lys Asp Ser Leu Pro
340 345 350
Val Cys Pro Val Asp Ala Ser Gly Cys Phe Thr Thr Glu Val Thr Asp
355 360 365
Phe Ala Gly Gln Tyr Val Lys Asp Ala Asp Lys Ser Ile Ile Arg Thr
370 375 380
Leu Lys Glu Gln Gly Arg Leu Leu Val Ala Thr Thr Phe Thr His Ser
385 390 395 400
Tyr Pro Phe Cys Trp Arg Ser Asp Thr Pro Leu Ile Tyr Lys Ala Val
405 410 415

Pro Ser Trp Phe Val Arg Val Glu Asn Met Val Asp Gln Leu Leu Arg
 420 425 430
 Asn Asn Asp Leu Cys Tyr Trp Val Pro Glu Leu Val Arg Glu Lys Arg
 435 440 445
 Phe Gly Asn Trp Leu Lys Asp Ala Arg Asp Trp Thr Ile Ser Arg Asn
 450 455 460
 Arg Tyr Trp Gly Thr Pro Ile Pro Leu Trp Val Ser Asp Asp Phe Glu
 465 470 475 480
 Glu Val Val Cys Ile Gly Ser Val Ala Glu Leu Glu Glu Leu Ser Gly
 485 490 495
 Ala Lys Ile Ser Asp Leu His Arg Glu Ser Val Asp His Leu Thr Ile
 500 505 510
 Pro Ser Arg Cys Gly Lys Gly Ser Leu His Arg Ile Ser Glu Val Phe
 515 520 525
 Asp Cys Trp Phe Glu Ser Gly Ser Met Pro Tyr Ala Gln Val His Tyr
 530 535 540
 Pro Phe Glu Asn Lys Arg Glu Phe Glu Asp Ala Phe Pro Ala Asp Phe
 545 550 555 560
 Ile Ala Glu Gly Ile Asp Gln Thr Arg Gly Trp Phe Tyr Thr Leu Leu
 565 570 575
 Val Leu Ala Thr Ala Leu Phe Gly Gln Pro Pro Phe Lys Asn Val Ile
 580 585 590
 Val Asn Gly Leu Val Leu Ala Ser Asp Gly Gln Lys Met Ser Lys Arg
 595 600 605
 Lys Lys Asn Tyr Pro Asp Pro Val Ser Ile Ile Gln Lys Tyr Gly Ala
 610 615 620
 Asp Ala Leu Arg Leu Tyr Leu Ile Asn Ser Pro Val Val Arg Ala Glu
 625 630 635 640
 Asn Leu Arg Phe Lys Glu Glu Gly Val Arg Asp Val Leu Lys Asp Val
 645 650 655
 Leu Leu Pro Trp Tyr Asn Ala Tyr Arg Phe Leu Ile Gln Asn Val Leu
 660 665 670
 Arg Leu Gln Lys Glu Glu Glu Ile Glu Phe Leu Tyr Asn Glu Asn Thr
 675 680 685
 Val Arg Glu Ser Pro Asn Ile Thr Asp Arg Trp Ile Leu Ser Phe Met
 690 695 700
 Gln Ser Leu Ile Gly Phe Phe Glu Thr Glu Met Ala Ala Tyr Arg Leu
 705 710 715 720
 Tyr Thr Val Val Pro Arg Leu Val Lys Phe Val Asp Ile Leu Thr Asn
 725 730 735

Trp Tyr Val Arg Met Asn Arg Arg Arg Leu Lys Gly Glu Asn Gly Met
740 745 750

Glu Asp Cys Val Met Ala Leu Glu Thr Leu Phe Ser Val Leu Leu Ser
755 760 765

Leu Cys Arg Leu Met Ala Pro Tyr Thr Pro Phe Leu Thr Glu Leu Met
770 775 780

Tyr Gln Asn Leu Lys Val Leu Ile Asp Pro Val Ser Val Gln Asp Lys
785 790 795 800

Asp Thr Leu Ser Ile His Tyr Leu Met Leu Pro Arg Val Arg Glu Glu
805 810 815

Leu Ile Asp Lys Lys Thr Glu Ser Ala Val Ser Gln Met Gln Ser Val
820 825 830

Ile Glu Leu Gly Arg Val Ile Arg Asp Arg Lys Thr Ile Pro Ile Lys
835 840 845

Tyr Pro Leu Lys Glu Ile Val Val Ile His Gln Asp Pro Glu Ala Leu
850 855 860

Lys Asp Ile Lys Ser Leu Glu Lys Tyr Ile Ile Glu Glu Leu Asn Val
865 870 875 880

Arg Lys Val Thr Leu Ser Thr Asp Lys Asn Lys Tyr Gly Ile Arg Leu
885 890 895

Arg Ala Glu Pro Asp His Met Val Leu Gly Lys Arg Leu Lys Gly Ala
900 905 910

Phe Lys Ala Val Met Thr Ser Ile Lys Gln Leu Ser Ser Glu Glu Leu
915 920 925

Glu Gln Phe Gln Lys Thr Gly Thr Ile Val Val Glu Gly His Glu Leu
930 935 940

His Asp Glu Asp Ile Arg Leu Met Tyr Thr Phe Asp Gln Ala Thr Gly
945 950 955 960

Gly Thr Ala Gln Phe Glu Ala His Ser Asp Ala Gln Ala Leu Val Leu
965 970 975

Leu Asp Val Thr Pro Asp Gln Ser Met Val Asp Glu Gly Met Ala Arg
980 985 990

Glu Val Ile Asn Arg Ile Gln Lys Leu Arg Lys Lys Cys Asn Leu Val
995 1000 1005

Pro Thr Asp Glu Ile Thr Val Tyr Tyr Lys Ala Lys Ser Glu Gly Thr
1010 1015 1020

Tyr Leu Asn Ser Val Ile Glu Ser His Thr Glu Phe Ile Phe Thr Thr
1025 1030 1035 1040

Ile Lys Ala Pro Leu Lys Pro Tyr Pro Val Ser Pro Ser Asp Lys Val
1045 1050 1055

Leu Ile Gln Glu Lys Thr Gln Leu Lys Gly Ser Glu Leu Glu Ile Thr
 1060 1065 1070
 Leu Thr Arg Gly Ser Ser Leu Pro Gly Pro Ala Cys Ala Tyr Val Asn
 1075 1080 1085
 Leu Asn Ile Cys Ala Asn Gly Ser Glu Gln Gly Gly Val Leu Leu Leu
 1090 1095 1100
 Glu Asn Pro Lys Gly Asp Asn Arg Leu Asp Leu Leu Lys Leu Lys Ser
 1105 1110 1115 1120
 Val Val Thr Ser Ile Phe Gly Val Lys Asn Thr Glu Leu Ala Val Phe
 1125 1130 1135
 His Asp Glu Thr Glu Ile Gln Asn Gln Thr Asp Leu Leu Ser Leu Ser
 1140 1145 1150
 Gly Lys Thr Leu Cys Val Thr Ala Gly Ser Ala Pro Ser Leu Ile Asn
 1155 1160 1165
 Ser Ser Ser Thr Leu Leu Cys Gln Tyr Ile Asn Leu Gln Leu Leu Asn
 1170 1175 1180
 Ala Lys Pro Gln Glu Cys Leu Met Gly Thr Val Gly Thr Leu Leu Leu
 1185 1190 1195 1200
 Glu Asn Pro Leu Gly Gln Asn Gly Leu Thr His Gln Gly Leu Leu Tyr
 1205 1210 1215
 Glu Ala Ala Lys Val Phe Gly Leu Arg Ser Arg Lys Leu Lys Leu Phe
 1220 1225 1230
 Leu Asn Glu Thr Gln Thr Gln Glu Ile Thr Glu Asp Ile Pro Val Lys
 1235 1240 1245
 Thr Leu Asn Met Lys Thr Val Tyr Val Ser Val Leu Pro Thr Thr Ala
 1250 1255 1260
 Asp Phe
 1265
 <210> 33
 <211> 1262
 <212> PRT
 <213> Homo sapiens
 <400> 33
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 1 5 10 15
 Lys Ile Leu Glu Phe Trp Thr Glu Phe Asn Cys Phe Gln Glu Cys Leu
 20 25 30
 Lys Gln Ser Lys His Lys Pro Lys Phe Thr Phe Tyr Asp Gly Pro Pro
 35 40 45
 Phe Ala Thr Gly Leu Pro His Tyr Gly His Ile Leu Ala Gly Thr Ile
 50 55 60

Lys Asp Ile Val Thr Arg Tyr Ala His Gln Ser Gly Phe His Val Asp
 65 70 75 80
 Arg Arg Phe Gly Trp Asp Cys His Gly Leu Pro Val Glu Tyr Glu Ile
 85 90 95
 Asp Lys Thr Leu Gly Ile Arg Gly Pro Glu Asp Val Ala Lys Met Gly
 100 105 110
 Ile Thr Glu Tyr Asn Asn Gln Cys Arg Ala Ile Val Met Arg Tyr Ser
 115 120 125
 Ala Glu Trp Lys Ser Thr Val Ser Arg Leu Gly Arg Trp Ile Asp Phe
 130 135 140
 Asp Asn Asp Tyr Lys Thr Leu Tyr Pro Gln Phe Met Glu Ser Val Trp
 145 150 155 160
 Trp Val Phe Lys Gln Leu Tyr Asp Lys Gly Leu Val Tyr Arg Gly Val
 165 170 175
 Lys Val Met Pro Phe Ser Thr Ala Cys Asn Thr Pro Leu Ser Asn Phe
 180 185 190
 Glu Ser His Gln Asn Tyr Lys Asp Val Gln Asp Pro Ser Val Phe Val
 195 200 205
 Thr Phe Pro Leu Glu Asp Glu Thr Val Ser Leu Val Ala Trp Thr
 210 215 220
 Thr Thr Pro Trp Thr Leu Pro Ser Asn Leu Ala Val Cys Val Asn Pro
 225 230 235 240
 Glu Met Gln Tyr Val Lys Ile Lys Asp Val Ala Arg Gly Arg Leu Leu
 245 250 255
 Ile Leu Met Glu Ala Arg Leu Ser Ala Leu Tyr Lys Leu Glu Ser Asp
 260 265 270
 Tyr Glu Ile Leu Glu Arg Phe Pro Gly Ala Tyr Leu Lys Gly Lys Lys
 275 280 285
 Tyr Arg Pro Leu Phe Asp Tyr Phe Leu Lys Cys Lys Glu Asn Gly Ala
 290 295 300
 Phe Thr Val Leu Val Asp Asn Tyr Val Lys Glu Glu Gly Thr Gly
 305 310 315 320
 Val Val His Gln Ala Pro Tyr Phe Gly Ala Glu Asp Tyr Arg Val Cys
 325 330 335
 Met Asp Phe Asn Ile Ile Arg Lys Asp Ser Leu Pro Val Cys Pro Val
 340 345 350
 Asp Ala Ser Gly Cys Phe Thr Thr Glu Val Thr Asp Phe Ala Gly Gln
 355 360 365
 Tyr Val Lys Asp Ala Asp Lys Ser Ile Ile Arg Thr Leu Lys Glu Gln
 370 375 380

Gly Arg Leu Leu Val Ala Thr Thr Phe Thr His Ser Tyr Pro Phe Cys
 385 390 395 400
 Trp Arg Ser Asp Thr Pro Leu Ile Tyr Lys Ala Val Pro Ser Trp Phe
 405 410 415
 Val Arg Val Glu Asn Met Val Asp Gln Leu Leu Arg Asn Asn Asp Leu
 420 425 430
 Cys Tyr Trp Val Pro Glu Leu Val Arg Glu Lys Arg Phe Gly Asn Trp
 435 440 445
 Leu Lys Asp Ala Arg Asp Trp Thr Ile Ser Arg Asn Arg Tyr Trp Gly
 450 455 460
 Thr Pro Ile Pro Leu Trp Val Ser Asp Asp Phe Glu Glu Val Val Cys
 465 470 475 480
 Ile Gly Ser Val Ala Glu Leu Glu Glu Leu Ser Gly Ala Lys Ile Ser
 485 490 495
 Asp Leu His Arg Glu Ser Val Asp His Leu Thr Ile Pro Ser Arg Cys
 500 505 510
 Gly Lys Gly Ser Leu His Arg Ile Ser Glu Val Phe Asp Cys Trp Phe
 515 520 525
 Glu Ser Gly Ser Met Pro Tyr Ala Gln Val His Tyr Pro Phe Glu Asn
 530 535 540
 Lys Arg Glu Phe Glu Asp Ala Phe Pro Ala Asp Phe Ile Ala Glu Gly
 545 550 555 560
 Ile Asp Gln Thr Arg Gly Trp Phe Tyr Thr Leu Leu Val Leu Ala Thr
 565 570 575
 Ala Leu Phe Gly Gln Pro Pro Phe Lys Asn Val Ile Val Asn Gly Leu
 580 585 590
 Val Leu Ala Ser Asp Gly Gln Lys Met Ser Lys Arg Lys Lys Asn Tyr
 595 600 605
 Pro Asp Pro Val Ser Ile Ile Gln Lys Tyr Gly Ala Asp Ala Leu Arg
 610 615 620
 Leu Tyr Leu Ile Asn Ser Pro Val Val Arg Ala Glu Asn Leu Arg Phe
 625 630 635 640
 Lys Glu Glu Gly Val Arg Asp Val Leu Lys Asp Val Leu Leu Pro Trp
 645 650 655
 Tyr Asn Ala Tyr Arg Phe Leu Ile Gln Asn Val Leu Arg Leu Gln Lys
 660 665 670
 Glu Glu Glu Ile Glu Phe Leu Tyr Asn Glu Asn Thr Val Arg Glu Ser
 675 680 685
 Pro Asn Ile Thr Asp Arg Trp Ile Leu Ser Phe Met Gln Ser Leu Ile
 690 695 700

Gly Phe Phe Glu Thr Glu Met Ala Ala Tyr Arg Leu Tyr Thr Val Val
 705 710 715 720
 Pro Arg Leu Val Lys Phe Val Asp Ile Leu Thr Asn Trp Tyr Val Arg
 725 730 735
 Met Asn Arg Arg Arg Leu Lys Gly Glu Asn Gly Met Glu Asp Cys Val
 740 745 750
 Met Ala Leu Glu Thr Leu Phe Ser Val Leu Leu Ser Leu Cys Arg Leu
 755 760 765
 Ile Ala Pro Tyr Thr Pro Phe Leu Thr Glu Leu Met Tyr Gln Asn Leu
 770 775 780
 Lys Val Leu Ile Asp Pro Val Ser Val Gln Asp Lys Asp Thr Leu Ser
 785 790 795 800
 Ile His Tyr Leu Met Leu Pro Arg Val Arg Glu Glu Leu Ile Asp Lys
 805 810 815
 Lys Thr Glu Ser Ala Val Ser Gln Met Gln Ser Val Ile Glu Leu Gly
 820 825 830
 Arg Val Ile Arg Asp Arg Lys Thr Ile Pro Ile Lys Tyr Pro Leu Lys
 835 840 845
 Glu Ile Val Val Ile His Gln Asp Pro Glu Ala Leu Lys Asp Ile Lys
 850 855 860
 Ser Leu Glu Lys Tyr Ile Ile Glu Glu Leu Asn Val Arg Lys Val Thr
 865 870 875 880
 Leu Ser Thr Asp Lys Asn Lys Tyr Gly Ile Arg Leu Arg Ala Glu Pro
 885 890 895
 Asp His Met Val Leu Gly Lys Arg Leu Lys Gly Ala Phe Lys Ala Val
 900 905 910
 Met Thr Ser Ile Lys Gln Leu Ser Ser Glu Glu Leu Glu Gln Phe Gln
 915 920 925
 Lys Thr Gly Thr Ile Val Val Glu Gly His Glu Leu His Asp Glu Asp
 930 935 940
 Ile Arg Leu Met Tyr Thr Phe Asp Gln Ala Thr Gly Gly Thr Ala Gln
 945 950 955 960
 Phe Glu Ala His Ser Asp Ala Gln Ala Leu Val Leu Leu Asp Val Thr
 965 970 975
 Pro Asp Gln Ser Met Val Asp Glu Gly Met Ala Arg Glu Val Ile Asn
 980 985 990
 Arg Ile Gln Lys Leu Arg Lys Lys Cys Asn Leu Val Pro Thr Asp Glu
 995 1000 1005
 Ile Thr Val Tyr Tyr Lys Ala Lys Ser Glu Gly Thr Tyr Leu Asn Ser
 1010 1015 1020

Val Ile Glu Ser His Thr Glu Phe Ile Phe Thr Thr Ile Lys Ala Pro
 1025 1030 1035 1040
 Leu Lys Pro Tyr Pro Val Ser Pro Asp Lys Val Leu Ile Gln Glu
 1045 1050 1055
 Lys Thr Gln Leu Lys Gly Ser Glu Leu Glu Ile Thr Leu Thr Arg Gly
 1060 1065 1070
 Ser Ser Leu Pro Gly Pro Ala Cys Ala Tyr Val Asn Leu Asn Ile Cys
 1075 1080 1085
 Ala Asn Gly Ser Glu Gln Gly Gly Val Leu Leu Glu Asn Pro Lys
 1090 1095 1100
 Gly Asp Asn Arg Leu Asp Leu Leu Lys Leu Lys Ser Val Val Thr Ser
 1105 1110 1115 1120
 Ile Phe Gly Val Lys Asn Thr Glu Leu Ala Val Phe His Asp Glu Thr
 1125 1130 1135
 Glu Ile Gln Asn Gln Thr Asp Leu Leu Ser Leu Ser Gly Lys Thr Leu
 1140 1145 1150
 Cys Val Thr Ala Gly Ser Ala Pro Ser Leu Ile Asn Ser Ser Thr
 1155 1160 1165
 Leu Leu Cys Gln Tyr Ile Asn Leu Gln Leu Leu Asn Ala Lys Pro Gln
 1170 1175 1180
 Glu Cys Leu Met Gly Thr Val Gly Thr Leu Leu Leu Glu Asn Pro Leu
 1185 1190 1195 1200
 Gly Gln Asn Gly Leu Thr His Gln Gly Leu Leu Tyr Glu Ala Ala Lys
 1205 1210 1215
 Val Phe Gly Leu Arg Ser Arg Lys Leu Lys Leu Phe Leu Asn Glu Thr
 1220 1225 1230
 Gln Thr Gln Glu Ile Thr Glu Asp Ile Pro Val Lys Thr Leu Asn Met
 1235 1240 1245
 Lys Thr Val Tyr Val Ser Val Leu Pro Thr Thr Ala Asp Phe
 1250 1255 1260
 <210> 34
 <211> 626
 <212> PRT
 <213> Arabidopsis thaliana
 <400> 34
 Met Glu Gly Ala Ala Asp Gln Thr Thr Lys Ala Leu Ser Glu Leu Ala
 1 5 10 15
 Met Asp Ser Ser Thr Thr Leu Asn Ala Ala Glu Ser Ser Ala Gly Asp
 20 25 30
 Gly Ala Gly Pro Arg Ser Lys Asn Ala Leu Lys Lys Glu Gln Lys Met
 35 40 45

Lys Gln Lys Glu Glu Glu Lys Arg Arg Lys Asp Glu Glu Lys Ala Glu
50 55 60

Lys Ala Lys Gln Ala Pro Lys Ala Ser Ser Gln Lys Ala Val Ala Ala
65 70 75 80

Asp Asp Glu Glu Met Asp Ala Thr Gln Tyr Tyr Glu Asn Arg Leu Lys
85 90 95

Tyr Leu Ala Ala Glu Lys Ala Lys Gly Glu Asn Pro Tyr Pro His Lys
100 105 110

Phe Ala Val Ser Met Ser Ile Pro Lys Tyr Ile Glu Thr Tyr Gly Ser
115 120 125

Leu Asn Asn Gly Asp His Val Glu Asn Ala Glu Glu Ser Leu Ala Gly
130 135 140

Arg Ile Met Ser Lys Arg Ser Ser Ser Lys Leu Phe Phe Tyr Asp
145 150 155 160

Leu His Gly Asp Asp Phe Lys Val Gln Val Met Ala Asp Ala Ser Lys
165 170 175

Ser Gly Leu Asp Glu Ala Glu Phe Leu Lys Leu His Ser Asn Ala Lys
180 185 190

Arg Gly Asp Ile Val Gly Val Ile Gly Phe Pro Gly Lys Thr Lys Arg
195 200 205

Gly Glu Leu Ser Ile Phe Pro Arg Ser Phe Ile Leu Leu Ser His Cys
210 215 220

Leu His Met Met Pro Arg Lys Ala Asp Asn Val Asn Ala Lys Lys Pro
225 230 235 240

Glu Ile Trp Val Pro Gly Gln Thr Arg Asn Pro Glu Ala Tyr Val Leu
245 250 255

Lys Asp Gln Glu Ser Arg Tyr Arg Gln Arg His Leu Asp Met Ile Leu
260 265 270

Asn Val Glu Val Arg Gln Ile Phe Arg Thr Arg Ala Lys Ile Ile Ser
275 280 285

Tyr Val Arg Arg Phe Leu Asp Asn Lys Asn Phe Leu Glu Val Glu Thr
290 295 300

Pro Met Met Asn Met Ile Ala Gly Gly Ala Ala Ala Arg Pro Phe Val
305 310 315 320

Thr His His Asn Asp Leu Asp Met Arg Leu Tyr Met Arg Ile Ala Pro
325 330 335

Glu Leu Tyr Leu Lys Gln Leu Ile Val Gly Gly Leu Glu Arg Val Tyr
340 345 350

Glu Ile Gly Lys Gln Phe Arg Asn Glu Gly Ile Asp Leu Thr His Asn
355 360 365

Pro Glu Phe Thr Thr Cys Glu Phe Tyr Met Ala Phe Ala Asp Tyr Asn
 370 375 380
 Asp Leu Met Glu Met Thr Glu Val Met Leu Ser Gly Met Val Lys Glu
 385 390 395 400
 Leu Thr Gly Gly Tyr Lys Ile Lys Tyr Asn Ala Asn Gly Tyr Asp Lys
 405 410 415
 Asp Pro Ile Glu Ile Asp Phe Thr Pro Pro Phe Arg Arg Ile Glu Met
 420 425 430
 Ile Gly Glu Leu Glu Lys Val Ala Lys Leu Asn Ile Pro Lys Asp Leu
 435 440 445
 Ala Ser Glu Glu Ala Asn Lys Tyr Leu Ile Asp Ala Cys Ala Arg Phe
 450 455 460
 Asp Val Lys Cys Pro Pro Pro Gln Thr Thr Ala Arg Leu Leu Asp Lys
 465 470 475 480
 Leu Val Gly Glu Phe Leu Glu Pro Thr Cys Val Asn Pro Thr Phe Ile
 485 490 495
 Ile Asn Gln Pro Glu Ile Met Ser Pro Leu Ala Lys Trp His Arg Ser
 500 505 510
 Lys Ser Gly Leu Thr Glu Arg Phe Glu Leu Phe Ile Asn Lys His Glu
 515 520 525
 Leu Cys Asn Ala Tyr Thr Glu Leu Asn Asp Pro Val Val Gln Arg Gln
 530 535 540
 Arg Phe Ala Asp Gln Leu Lys Asp Arg Gln Ser Gly Asp Asp Glu Ala
 545 550 555 560
 Met Ala Leu Asp Glu Thr Phe Cys Asn Ala Leu Glu Tyr Gly Leu Ala
 565 570 575
 Pro Thr Gly Gly Trp Gly Leu Gly Ile Asp Arg Leu Ser Met Leu Leu
 580 585 590
 Thr Asp Ser Leu Asn Ile Lys Glu Val Leu Phe Phe Pro Ala Met Arg
 595 600 605
 Pro Pro Gln Glu Glu Ser Ala Ala Ala Gln Ala Pro Leu Thr Glu Glu
 610 615 620
 Lys Lys
 625
 <210> 35
 <211> 451
 <212> PRT
 <213> Homo sapiens
 <400> 35
 Met Val Gly Ser Ala Leu Arg Arg Gly Ala His Ala Tyr Val Tyr Leu
 1 5 10 15

Val Ser Lys Ala Ser His Ile Ser Arg Gly His Gln His Gln Ala Trp
 20 25 30
 Gly Ser Arg Pro Pro Ala Ala Glu Cys Ala Thr Gln Arg Ala Pro Gly
 35 40 45
 Ser Val Val Glu Leu Leu Gly Lys Ser Tyr Pro Gln Asp Asp His Ser
 50 55 60
 Asn Leu Thr Arg Lys Val Leu Thr Arg Val Gly Arg Asn Leu His Asn
 65 70 75 80
 Gln Gln His His Pro Leu Trp Leu Ile Lys Glu Arg Val Lys Glu His
 85 90 95
 Phe Tyr Lys Gln Tyr Val Gly Arg Phe Gly Thr Pro Leu Phe Ser Val
 100 105 110
 Tyr Asp Asn Leu Ser Pro Val Val Thr Thr Trp Gln Asn Phe Asp Ser
 115 120 125
 Leu Leu Ile Pro Ala Asp His Pro Ser Arg Lys Lys Gly Asp Asn Tyr
 130 135 140
 Tyr Leu Asn Arg Thr His Met Leu Arg Ala His Thr Ser Ala His Gln
 145 150 155 160
 Trp Asp Leu Leu His Ala Gly Leu Asp Ala Phe Leu Val Val Gly Asp
 165 170 175
 Val Tyr Arg Arg Asp Gln Ile Asp Ser Gln His Tyr Pro Ile Phe His
 180 185 190
 Gln Leu Glu Ala Val Arg Leu Phe Ser Lys His Glu Leu Phe Ala Gly
 195 200 205
 Ile Lys Asp Gly Glu Ser Leu Gln Leu Phe Glu Gln Ser Ser Arg Ser
 210 215 220
 Ala His Lys Gln Glu Thr His Thr Met Glu Ala Val Lys Leu Val Glu
 225 230 235 240
 Phe Asp Leu Lys Gln Thr Leu Thr Arg Leu Met Ala His Leu Phe Gly
 245 250 255
 Asp Glu Leu Glu Ile Arg Trp Val Asp Cys Tyr Phe Pro Phe Thr His
 260 265 270
 Pro Ser Phe Glu Met Glu Ile Asn Phe His Gly Glu Trp Leu Glu Val
 275 280 285
 Leu Gly Cys Gly Val Met Glu Gln Gln Leu Val Asn Ser Ala Gly Ala
 290 295 300
 Gln Asp Arg Ile Gly Trp Ala Phe Gly Leu Gly Leu Glu Arg Leu Ala
 305 310 315 320
 Met Ile Leu Tyr Asp Ile Pro Asp Ile Arg Leu Phe Trp Cys Glu Asp
 325 330 335

Glu Arg Phe Leu Lys Gln Phe Cys Val Ser Asn Ile Asn Gln Lys Val
 340 345 350
 Lys Phe Gln Pro Leu Ser Lys Tyr Pro Ala Val Ile Asn Asp Ile Ser
 355 360 365
 Phe Trp Leu Pro Ser Glu Asn Tyr Ala Glu Asn Asp Phe Tyr Asp Leu
 370 375 380
 Val Arg Thr Ile Gly Gly Asp Leu Val Glu Lys Val Asp Leu Ile Asp
 385 390 395 400
 Lys Phe Val His Pro Lys Thr His Lys Thr Ser His Cys Tyr Arg Ile
 405 410 415
 Thr Tyr Arg His Met Glu Arg Thr Leu Ser Gln Arg Glu Val Arg His
 420 425 430
 Ile His Gln Ala Leu Gln Glu Ala Ala Val Gln Leu Leu Gly Val Glu
 435 440 445
 Gly Arg Phe
 450
 <210> 36
 <211> 503
 <212> PRT
 <213> Saccharomyces cerevisiae
 <400> 36
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 1 5 10 15
 Glu Ile Lys Ser Thr Leu Ala Thr Phe Pro Gln His Gly Ser Gln Asp
 20 25 30
 Val Leu Ser Ala Leu Asn Ser Leu Lys Ala His Asn Lys Leu Glu Phe
 35 40 45
 Ser Lys Val Asp Thr Val Thr Tyr Asp Leu Thr Lys Glu Gly Ala Gln
 50 55 60
 Ile Leu Asn Glu Gly Ser Tyr Glu Ile Lys Leu Val Lys Leu Ile Gln
 65 70 75 80
 Glu Leu Gly Gln Leu Gln Ile Lys Asp Val Met Ser Lys Leu Gly Pro
 85 90 95
 Gln Val Gly Lys Val Gly Gln Ala Arg Ala Phe Lys Asn Gly Trp Ile
 100 105 110
 Ala Lys Asn Ala Ser Asn Glu Leu Glu Leu Ser Ala Lys Leu Gln Asn
 115 120 125
 Thr Asp Leu Asn Glu Leu Thr Asp Glu Thr Gln Ser Ile Leu Ala Gln
 130 135 140
 Ile Lys Asn Asn Ser His Leu Asp Ser Ile Asp Ala Lys Ile Leu Asn
 145 150 155 160

Asp Leu Lys Lys Arg Lys Leu Ile Ala Gln Gly Lys Ile Thr Asp Phe
 165 170 175
 Ser Val Thr Lys Gly Pro Glu Phe Ser Thr Asp Leu Thr Lys Leu Glu
 180 185 190
 Thr Asp Leu Thr Ser Asp Met Val Ser Thr Asn Ala Tyr Lys Asp Leu
 195 200 205
 Lys Phe Lys Pro Tyr Asn Phe Asn Ser Gln Gly Val Gln Ile Ser Ser
 210 215 220
 Gly Ala Leu His Pro Leu Asn Lys Val Arg Glu Glu Phe Arg Gln Ile
 225 230 235 240
 Phe Phe Ser Met Gly Phe Thr Glu Met Pro Ser Asn Gln Tyr Val Glu
 245 250 255
 Thr Gly Phe Trp Asn Phe Asp Ala Leu Tyr Val Pro Gln Gln His Pro
 260 265 270
 Ala Arg Asp Leu Gln Asp Thr Phe Tyr Ile Lys Asp Pro Leu Thr Ala
 275 280 285
 Glu Leu Pro Asp Asp Lys Thr Tyr Met Asp Asn Ile Lys Ala Val His
 290 295 300
 Glu Gln Gly Arg Phe Gly Ser Ile Gly Tyr Arg Tyr Asn Trp Lys Pro
 305 310 315 320
 Glu Glu Cys Gln Lys Leu Val Leu Arg Thr His Ser Thr Ala Ile Ser
 325 330 335
 Ala Arg Met Leu His Asp Leu Ala Lys Asp Pro Lys Pro Thr Arg Leu
 340 345 350
 Phe Ser Ile Asp Arg Val Phe Arg Asn Glu Ala Val Asp Ala Thr His
 355 360 365
 Leu Ala Glu Phe His Gln Val Glu Gly Val Leu Ala Asp Tyr Asn Ile
 370 375 380
 Thr Leu Gly Asp Leu Ile Lys Phe Met Glu Glu Phe Phe Glu Arg Met
 385 390 395 400
 Gly Val Thr Gly Leu Arg Phe Lys Pro Thr Tyr Asn Pro Tyr Thr Glu
 405 410 415
 Pro Ser Met Glu Ile Phe Ser Trp His Glu Gly Leu Gln Lys Trp Val
 420 425 430
 Glu Ile Gly Asn Ser Gly Met Phe Arg Pro Glu Met Leu Glu Ser Met
 435 440 445
 Gly Leu Pro Lys Asp Leu Arg Val Leu Gly Trp Gly Leu Ser Leu Glu
 450 455 460
 Arg Pro Thr Met Ile Lys Tyr Lys Val Gln Asn Ile Arg Glu Leu Leu
 465 470 475 480

Gly His Lys Val Ser Leu Asp Phe Ile Glu Thr Asn Pro Ala Ala Arg
 485 490 495
 Leu Asp Glu Asp Leu Tyr Glu
 500

<210> 37
 <211> 1440
 <212> PRT
 <213> Homo sapiens

<400> 37 Met Glu His Thr Glu Ile Asp His Trp Leu Glu Phe Ser Ala Thr Lys
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 1 Leu Ser Ser Cys Asp Ser Phe Thr Ser Thr Ile Asn Glu Leu Asn His
 30 25
 20 Cys Leu Ser Leu Arg Thr Tyr Leu Val Gly Asn Ser Leu Ser Leu Ala
 45 35 40
 50 Asp Leu Cys Val Trp Ala Thr Leu Lys Gly Asn Ala Ala Trp Gln Glu
 60 55
 65 Gln Leu Lys Gln Lys Ala Pro Val His Val Lys Arg Trp Phe Gly
 80 70 75
 Phe Leu Glu Ala Gln Gln Ala Phe Gln Ser Val Gly Thr Lys Trp Asp
 95 85 90
 100 Val Ser Thr Thr Lys Ala Arg Val Ala Pro Glu Lys Lys Gln Asp Val
 110 105
 115 Gly Lys Phe Val Glu Leu Pro Gly Ala Glu Met Gly Lys Val Thr Val
 125 120
 130 Arg Phe Pro Pro Glu Ala Ser Gly Tyr Leu His Ile Gly His Ala Lys
 140 135
 145 Ala Ala Leu Leu Asn Gln His Tyr Gln Val Asn Phe Lys Gly Lys Leu
 160 150 155
 Ile Met Arg Phe Asp Asp Thr Asn Pro Glu Lys Glu Lys Glu Asp Phe
 175 165 170
 180 Glu Lys Val Ile Leu Glu Asp Val Ala Met Leu His Ile Lys Pro Asp
 185
 190 Gln Phe Thr Tyr Thr Ser Asp His Phe Glu Thr Ile Met Lys Tyr Ala
 205 195 200
 210 Glu Lys Leu Ile Gln Glu Gly Lys Ala Tyr Val Asp Asp Thr Pro Ala
 220 215
 225 Glu Gln Met Lys Ala Glu Arg Glu Gln Arg Ile Glu Ser Lys His Arg
 240 230 235
 Lys Asn Pro Ile Glu Lys Asn Leu Gln Met Trp Glu Glu Met Lys Lys
 255 245 250

Gly Ser Gln Phe Gly His Ser Cys Cys Leu Arg Ala Lys Ile Asp Met
260 265 270

Ser Ser Asn Asn Gly Cys Met Arg Asp Pro Thr Leu Tyr Arg Cys Lys
275 280 285

Ile Gln Pro His Pro Arg Thr Gly Asn Lys Tyr Asn Val Tyr Pro Thr
290 295 300

Tyr Asp Phe Ala Cys Pro Ile Val Asp Ser Ile Glu Gly Val Thr His
305 310 315 320

Ala Leu Arg Thr Thr Glu Tyr His Asp Arg Asp Glu Gln Phe Tyr Trp
325 330 335

Ile Ile Glu Ala Leu Gly Ile Arg Lys Pro Tyr Ile Trp Glu Tyr Ser
340 345 350

Arg Leu Asn Leu Asn Asn Thr Val Leu Ser Lys Arg Lys Leu Thr Trp
355 360 365

Phe Val Asn Glu Gly Leu Val Asp Gly Trp Asp Asp Pro Arg Phe Pro
370 375 380

Thr Val Arg Gly Val Leu Arg Arg Gly Met Thr Val Glu Gly Leu Lys
385 390 395 400

Gln Phe Ile Ala Ala Gln Gly Ser Ser Arg Ser Val Val Asn Met Glu
405 410 415

Trp Asp Lys Ile Trp Ala Phe Asn Lys Lys Val Ile Asp Pro Val Ala
420 425 430

Pro Arg Tyr Val Ala Leu Leu Lys Lys Glu Val Ile Pro Val Asn Val
435 440 445

Pro Glu Ala Gln Glu Glu Met Lys Glu Val Ala Lys His Pro Lys Asn
450 455 460

Pro Glu Val Gly Leu Lys Pro Val Trp Tyr Ser Pro Lys Val Phe Ile
465 470 475 480

Glu Gly Ala Asp Ala Glu Thr Phe Ser Glu Gly Glu Met Val Thr Phe
485 490 495

Ile Asn Trp Gly Asn Leu Asn Ile Thr Lys Ile His Lys Asn Ala Asp
500 505 510

Gly Lys Ile Ile Ser Leu Asp Ala Lys Phe Asn Leu Glu Asn Lys Asp
515 520 525

Tyr Lys Lys Thr Thr Lys Val Thr Trp Leu Ala Glu Thr Thr His Ala
530 535 540

Leu Pro Ile Pro Val Ile Cys Val Thr Tyr Glu His Leu Ile Thr Lys
545 550 555 560

Pro Val Leu Gly Lys Asp Glu Asp Phe Lys Gln Tyr Val Asn Lys Asn
565 570 575

Ser Lys His Glu Glu Leu Met Leu Gly Asp Pro Cys Leu Lys Asp Leu
580 585 590

Lys Lys Gly Asp Ile Ile Gln Leu Gln Arg Arg Gly Phe Phe Ile Cys
595 600 605

Asp Gln Pro Tyr Glu Pro Val Ser Pro Tyr Ser Cys Lys Glu Ala Pro
610 615 620

Cys Val Leu Ile Tyr Ile Pro Asp Gly His Thr Lys Glu Met Pro Thr
625 630 635 640

Ser Gly Ser Lys Glu Lys Thr Lys Val Glu Ala Thr Lys Asn Glu Thr
645 650 655

Ser Ala Pro Phe Lys Glu Arg Pro Thr Pro Ser Leu Asn Asn Asn Cys
660 665 670

Thr Thr Ser Glu Asp Ser Leu Val Leu Tyr Asn Arg Val Ala Val Gln
675 680 685

Gly Asp Val Val Arg Glu Leu Lys Ala Lys Lys Ala Pro Lys Glu Asp
690 695 700

Val Asp Ala Ala Val Lys Gln Leu Leu Ser Leu Lys Ala Glu Tyr Lys
705 710 715 720

Glu Lys Thr Gly Gln Glu Tyr Lys Pro Gly Asn Pro Pro Ala Glu Ile
725 730 735

Gly Gln Asn Ile Ser Ser Asn Ser Ala Ser Ile Leu Glu Ser Lys
740 745 750

Ser Leu Tyr Asp Glu Val Ala Ala Gln Gly Glu Val Val Arg Lys Leu
755 760 765

Lys Ala Glu Lys Ser Pro Lys Ala Lys Ile Asn Glu Ala Val Glu Cys
770 775 780

Leu Leu Ser Leu Lys Ala Gln Tyr Lys Glu Lys Thr Gly Lys Glu Tyr
785 790 795 800

Ile Pro Gly Gln Pro Pro Leu Ser Gln Ser Ser Asp Ser Ser Pro Thr
805 810 815

Arg Asn Ser Glu Pro Ala Gly Leu Glu Thr Pro Glu Ala Lys Val Leu
820 825 830

Phe Asp Lys Val Ala Ser Gln Gly Glu Val Val Arg Lys Leu Lys Thr
835 840 845

Glu Lys Ala Pro Lys Asp Gln Val Asp Ile Ala Val Gln Glu Leu Leu
850 855 860

Gln Leu Lys Ala Gln Tyr Lys Ser Leu Ile Gly Val Glu Tyr Lys Pro
865 870 875 880

Val Ser Ala Thr Gly Ala Glu Asp Lys Asp Lys Lys Lys Glu Lys
885 890 895

Gly Asn Asn Lys Ser Glu Lys Gln Asn Lys Pro Gln Lys Gln Asn Asp Gly
 900 905 910
 Gln Arg Lys Asp Pro Ser Lys Asn Gln Gly Gly Leu Ser Ser Ser
 915 920 925
 Gly Ala Gly Glu Gly Gln Gly Pro Lys Lys Gln Thr Arg Leu Gly Leu
 930 935 940
 Glu Ala Lys Lys Glu Glu Asn Leu Ala Asp Trp Tyr Ser Gln Val Ile
 945 950 955 960
 Thr Lys Ser Glu Met Ile Glu Tyr His Asp Ile Ser Gly Cys Tyr Ile
 965 970 975
 Leu Arg Pro Trp Ala Tyr Ala Ile Trp Glu Ala Ile Lys Asp Phe Phe
 980 985 990
 Asp Ala Glu Ile Lys Lys Leu Gly Val Glu Asn Cys Tyr Phe Pro Met
 995 1000 1005
 Phe Val Ser Gln Ser Ala Leu Glu Lys Glu Lys Thr His Val Ala Asp
 1010 1015 1020
 Phe Ala Pro Glu Val Ala Trp Val Thr Arg Ser Gly Lys Thr Glu Leu
 1025 1030 1035 1040
 Ala Glu Pro Ile Ala Ile Arg Pro Thr Ser Glu Thr Val Met Tyr Pro
 1045 1050 1055
 Ala Tyr Ala Lys Trp Val Gln Ser His Arg Asp Leu Pro Ile Lys Leu
 1060 1065 1070
 Asn Gln Trp Cys Asn Val Val Arg Trp Glu Phe Lys His Pro Gln Pro
 1075 1080 1085
 Phe Leu Arg Thr Arg Glu Phe Leu Trp Gln Glu Gly His Ser Ala Phe
 1090 1095 1100
 Ala Thr Met Glu Glu Ala Ala Glu Glu Val Leu Gln Ile Leu Asp Leu
 1105 1110 1115 1120
 Tyr Ala Gln Val Tyr Glu Glu Leu Leu Ala Ile Pro Val Val Lys Gly
 1125 1130 1135
 Arg Lys Thr Glu Lys Glu Lys Phe Ala Gly Asp Tyr Thr Thr Thr
 1140 1145 1150
 Ile Glu Ala Phe Ile Ser Ala Ser Gly Arg Ala Ile Gln Gly Gly Thr
 1155 1160 1165
 Ser His His Leu Gly Gln Asn Phe Ser Lys Met Phe Glu Ile Val Phe
 1170 1175 1180
 Glu Asp Pro Lys Ile Pro Gly Glu Lys Gln Phe Ala Tyr Gln Asn Ser
 1185 1190 1195 1200
 Trp Gly Leu Thr Thr Arg Thr Ile Gly Val Met Thr Met Val His Gly
 1205 1210 1215

Asp Asn Met Gly Leu Val Leu Pro Pro Arg Val Ala Cys Val Gln Val
1220 1225 1230
Val Ile Ile Pro Cys Gly Ile Thr Asn Ala Leu Ser Glu Glu Asp Lys
1235 1240 1245
Glu Ala Leu Ile Ala Lys Cys Asn Asp Tyr Arg Arg Arg Leu Leu Ser
1250 1255 1260
Val Asn Ile Arg Val Arg Ala Asp Leu Arg Asp Asn Tyr Ser Pro Gly
1265 1270 1275 1280
Trp Lys Phe Asn His Trp Glu Leu Lys Gly Val Pro Ile Arg Leu Glu
1285 1290 1295
Val Gly Pro Arg Asp Met Lys Ser Cys Gln Phe Val Ala Val Arg Arg
1300 1305 1310
Asp Thr Gly Glu Lys Leu Thr Val Ala Glu Asn Glu Ala Glu Thr Lys
1315 1320 1325
Leu Gln Ala Ile Leu Glu Asp Ile Gln Val Thr Leu Phe Thr Arg Ala
1330 1335 1340
Ser Glu Asp Leu Lys Thr His Met Val Val Ala Asn Thr Met Glu Asp
1345 1350 1355 1360
Phe Gln Lys Ile Leu Asp Ser Gly Lys Ile Val Gln Ile Pro Phe Cys
1365 1370 1375
Gly Glu Ile Asp Cys Glu Asp Trp Ile Lys Lys Thr Thr Ala Arg Asp
1380 1385 1390
Gln Asp Leu Glu Pro Gly Ala Pro Ser Met Gly Ala Lys Ser Leu Cys
1395 1400 1405
Ile Pro Phe Lys Pro Leu Cys Glu Leu Gln Pro Gly Ala Lys Cys Val
1410 1415 1420
Cys Gly Lys Asn Pro Ala Lys Tyr Tyr Thr Leu Phe Gly Arg Ser Tyr
1425 1430 1435 1440